Sheet 1 of 90
Appl. No. 10/677,754; Filed: Oct 3, 2003
Dkt No. 2060.0200003/HCC/PAC; Group Unit: To be assigned
Inventors: SETTE et al.
Tel. No.: 202-371-2600
For: Optimized Multi-Epitope Constructs and Uses Thereof

Immunogenicity of HIV-and HCV-derived minigenes in HLA transgenic animals.

ıde of CTL responses are shown as follows: + up to 2 LU (Lytic Units) or 10 SV (Secretory Units); ++ up to 200 LU or 100 SU; +++ up to 200 LU
0 Su; ++++more than 2009 LU or 1000 SU. Magnitude represents number of independent cultures yielding positive responses.

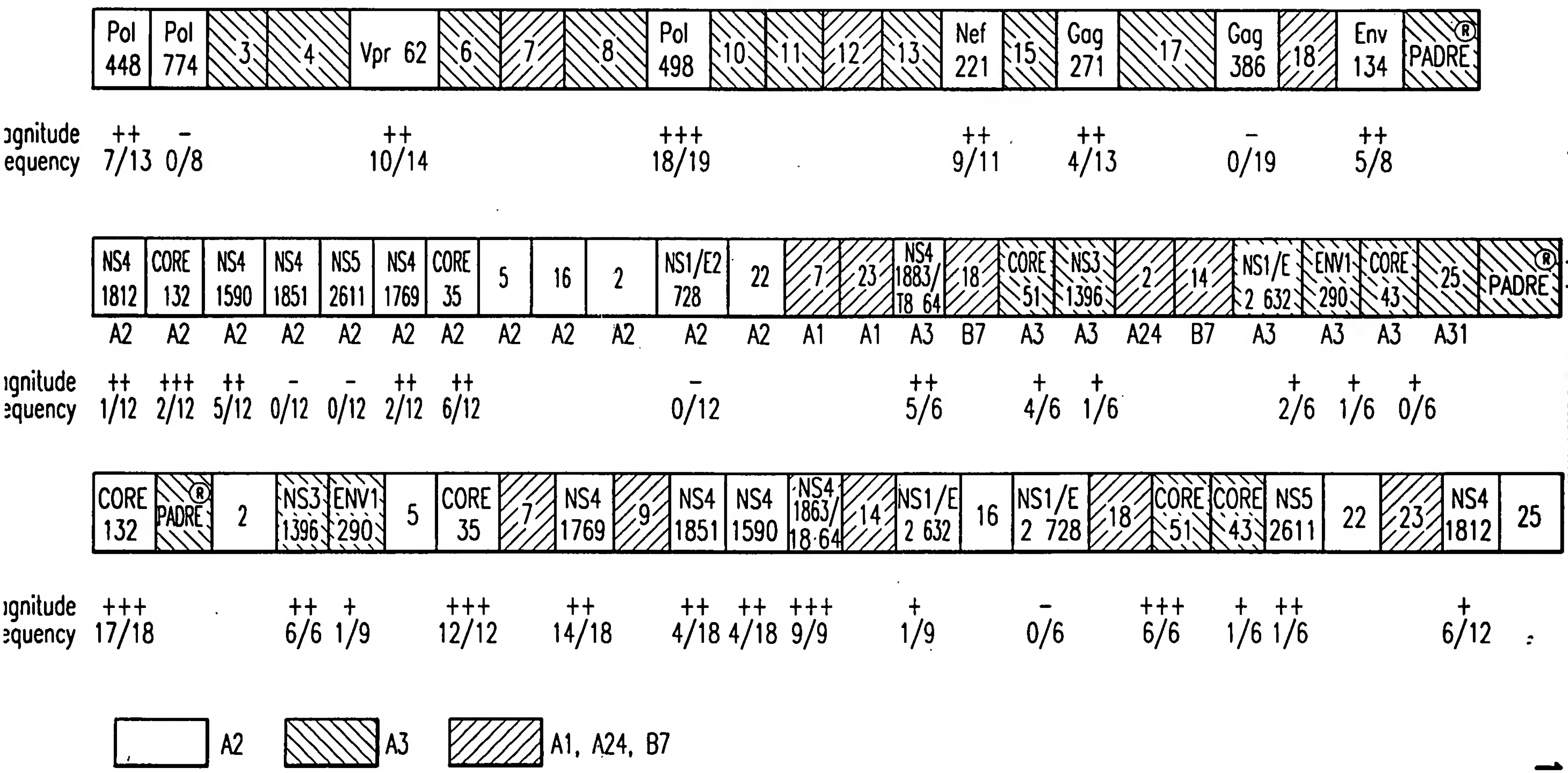
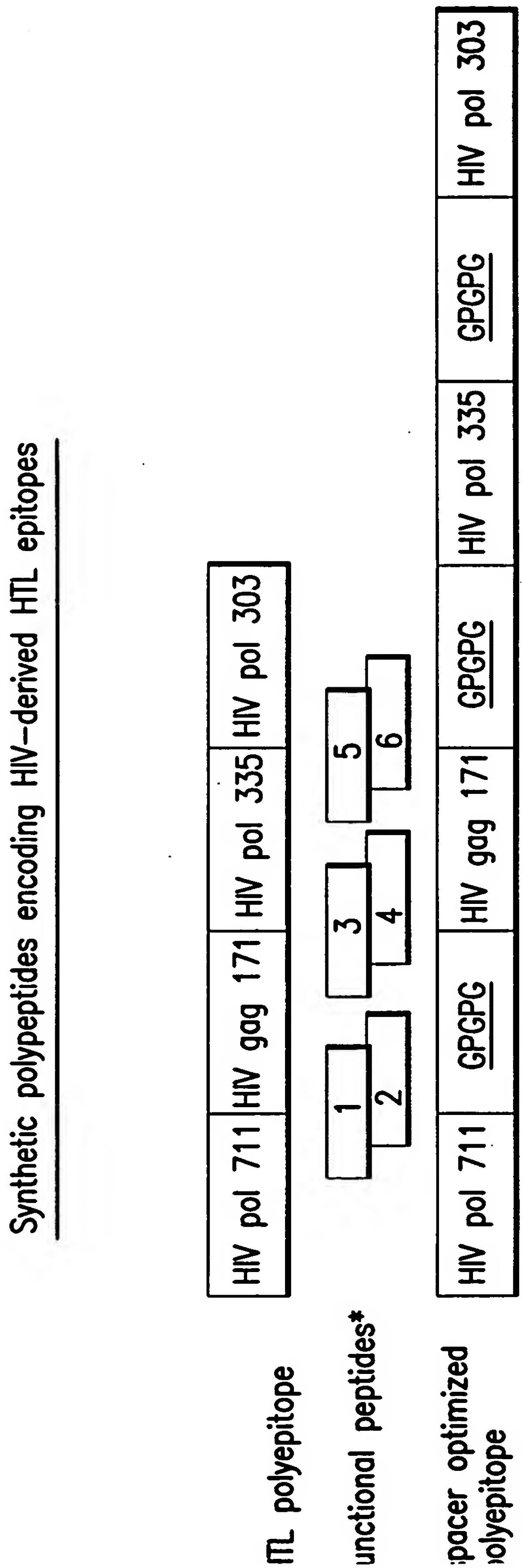


FIG. 1



ction peptides comprise either 10 amino acids from the N–terminal epitope and 5 amino acids from the
erminal epitope or 5 amino acids from the N–terminal epitope and 10 amino acids from the C–terminal epitope.

FIG.2A

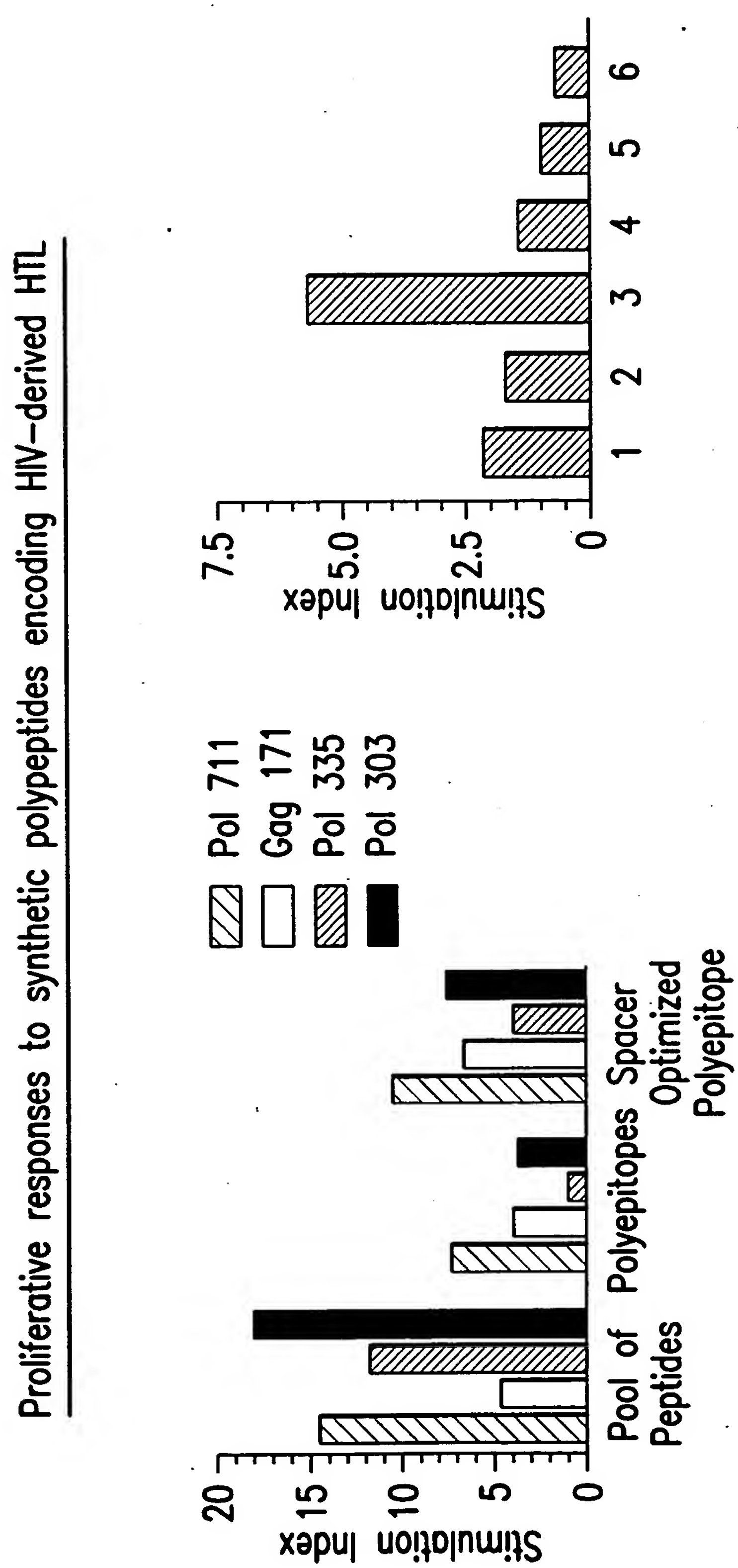

Proliferative responses to synthetic polypeptides encoding HIV-derived HTL
Stimulation Index
20
15
10
5
0
Pool of Peptides
Polyepitopes
Spacer Optimized Polyepitope
Pol 711
Gag 171
Pol 335
Pol 303
Stimulation Index
7.5
5.0
2.5
0
1
2
3
4
5
6

FIG.2B

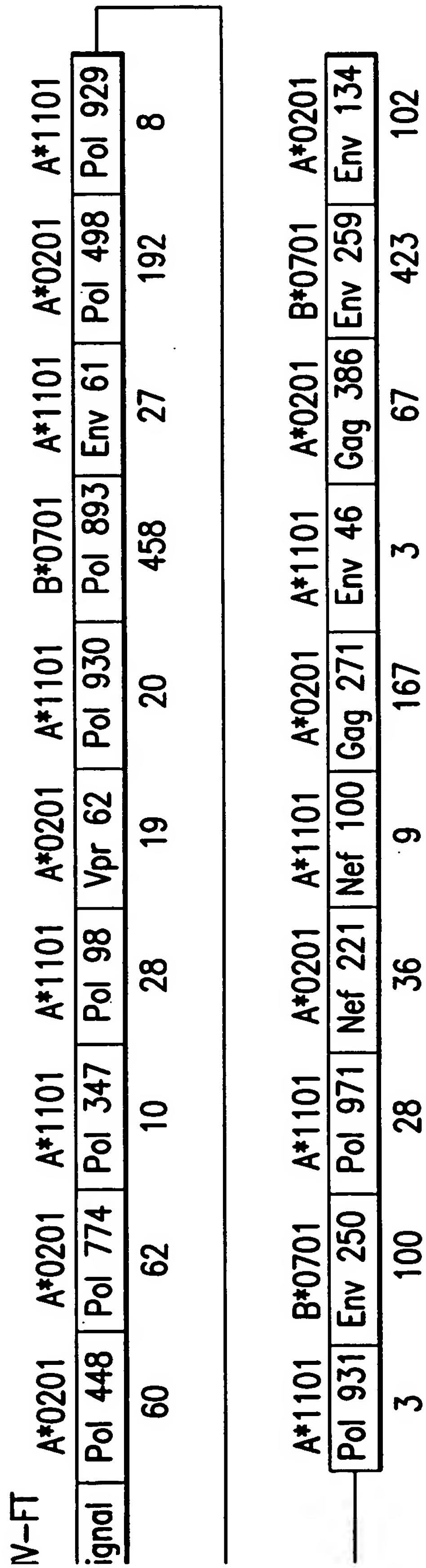

IV-FT
ignal
A*0201
Pol 448
60
A*0201
Pol 774
62
A*1101
Pol 347
10
A*1101
Pol 98
28
A*0201
Vpr 62
19
A*1101
Pol 930
20
B*0701
Pol 893
458
A*1101
Env 61
27
A*0201
Pol 498
192
A*1101
Pol 929
8
A*1101
Pol 931
3
B*0701
Env 250
100
A*1101
Pol 971
28
A*0201
Nef 221
36
A*1101
Nef 100
9
A*0201
Gag 271
167
A*1101
Env 46
3
A*0201
Gag 386
67
B*0701
Env 259
423
A*0201
Env 134
102

FIG.3A

–specific multiepitope constructs

.1

	A*1101		A*0201	A*0201	A*0201	A*0201	A*0201	A*1101	A*1101	A*0201
nal	pol 149	PADRE®	core 18	pol 562	pol 551	pol 455	env 183	core 141	pol 665	env 335
	14		2	8	5	76	10	4	11	5
			F							

.2

	A*1101		A*0201	A*1101	A*0201	A*0201	A*0201	A*0201	A*1101	A*1101	A*0201
nal	pol 149	PADRE®	core 18	pol 629	pol 562	pol 551	pol 455	env 183	core 141	pol 665	env 335
	14		2	353	8	5	76	10	4	11	5
			K								

.1X

	A*1101		A*0201		A*0201	A*0201	A*0201	A*0201	A*1101	A*1101	A*0201
nal	pol 149	PADRE®	core 18	C_1	pol 562	pol 551	pol 455	env 183	core 141	pol 665	env 335

C_1 = either W, Y, L, K, R, C, N or G

FIG.3B

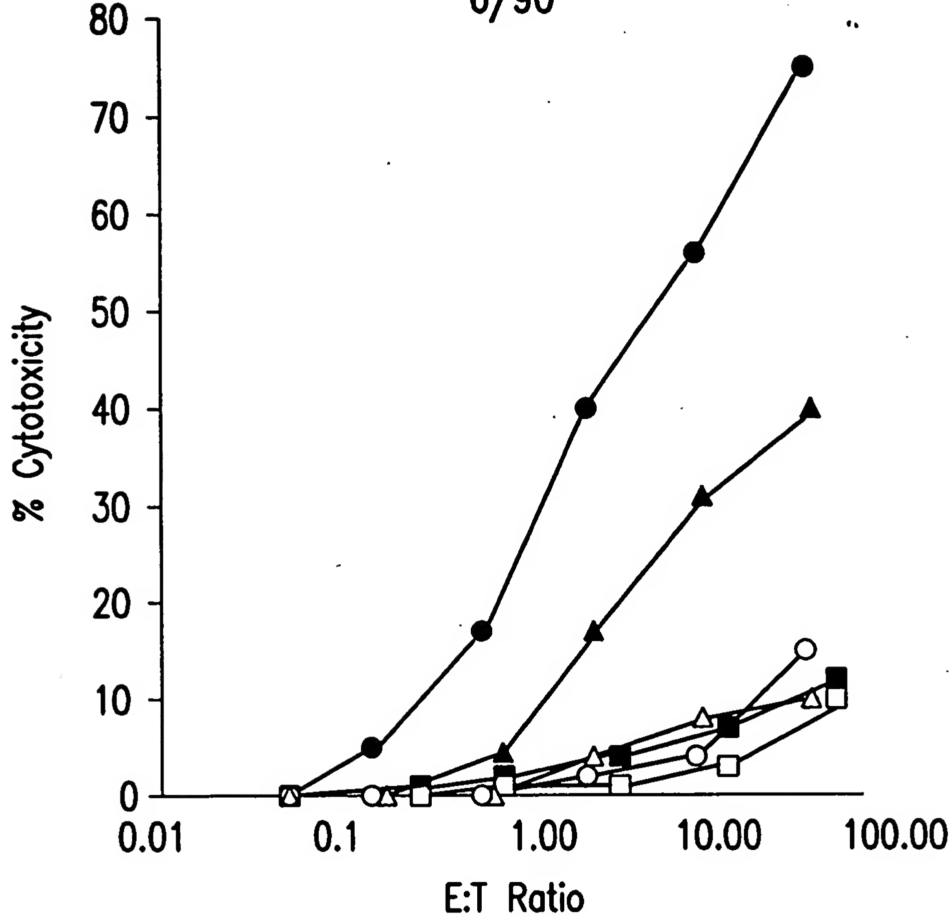
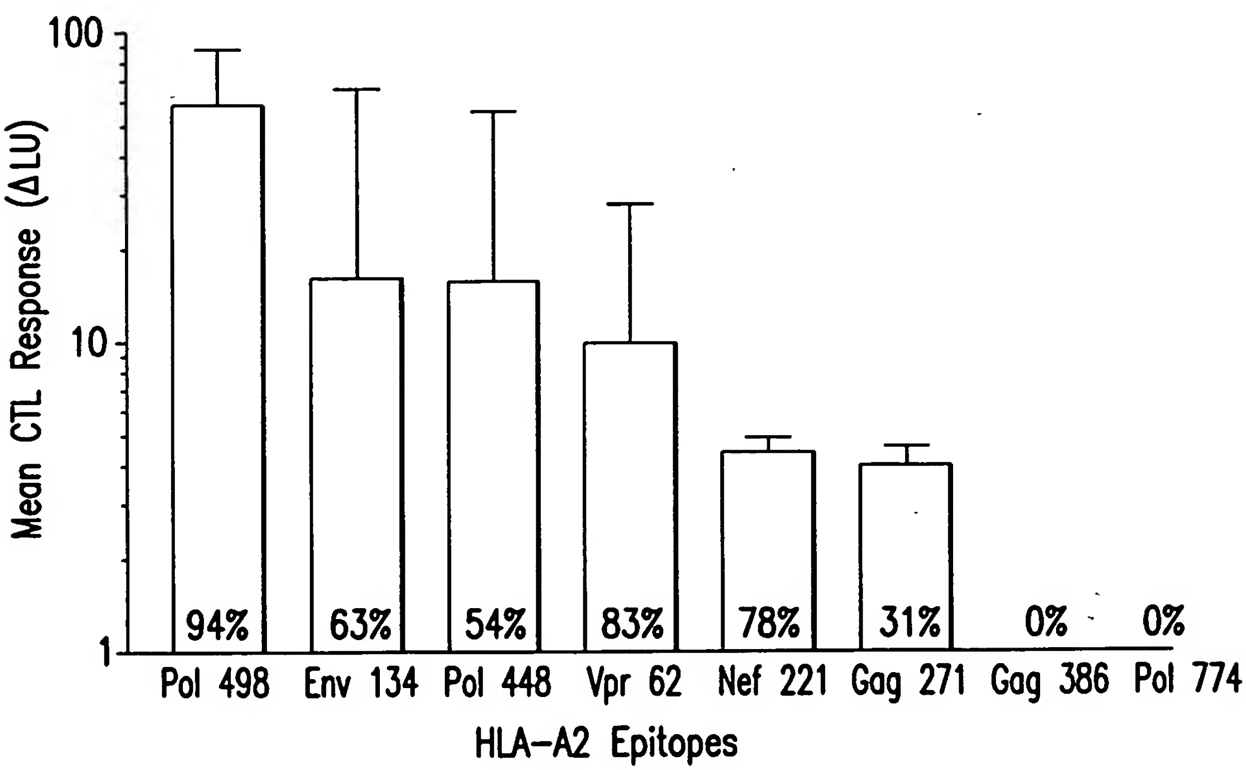

80
70
60
50
40
30
20
10
0
% Cytotoxicity
0.01
0.1
1.00
10.00
100.00
E:T Ratio

FIG.4A


100
10
1
Mean CTL Response (ΔLU)
94%
63%
54%
83%
78%
31%
0%
0%
Pol 498
Env 134
Pol 448
Vpr 62
Nef 221
Gag 271
Gag 386
Pol 774
HLA-A2 Epitopes

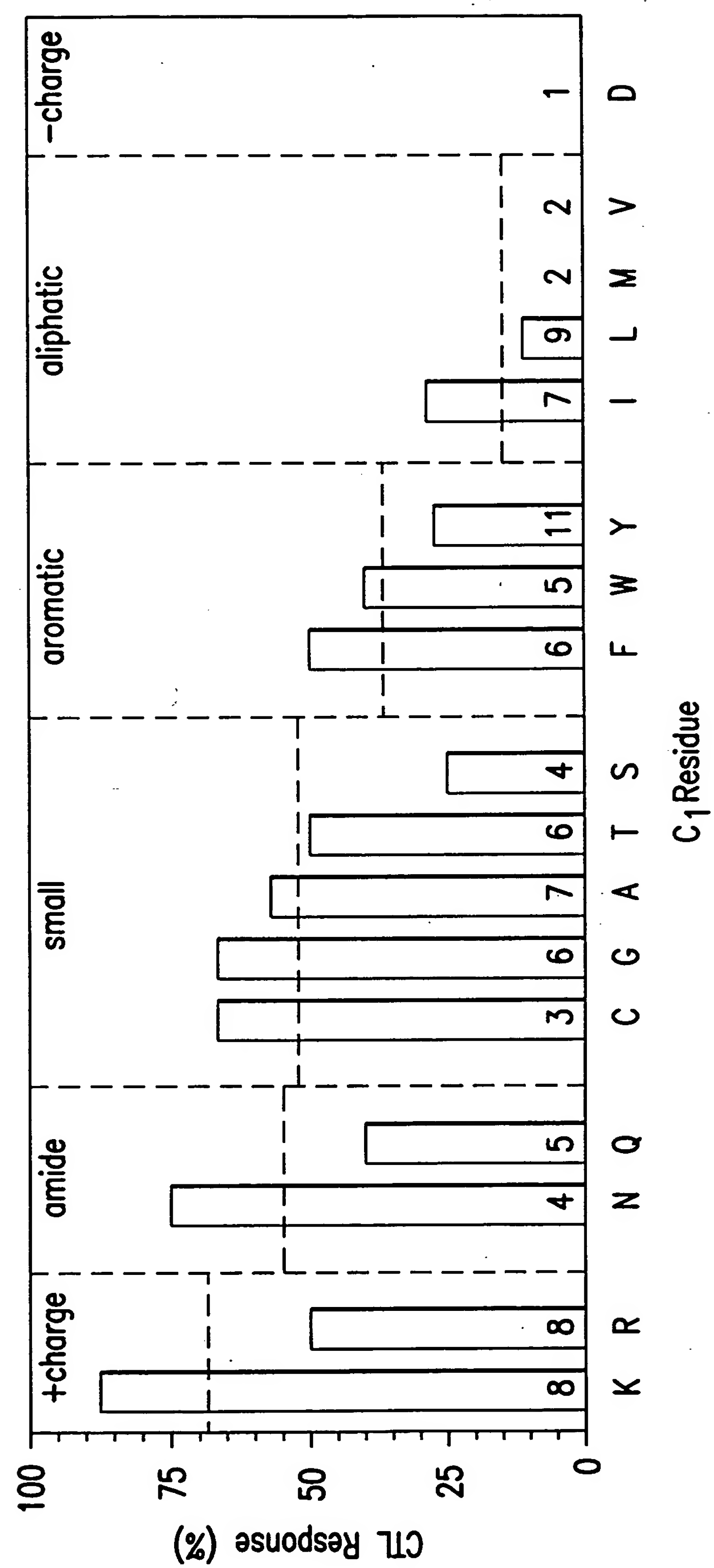

+charge
amide
small
aromatic
aliphatic
-charge
8
8
4
5
3
6
7
6
4
6
5
11
7
9
2
2
1
K
R
N
Q
C
G
A
T
S
F
W
Y
I
L
M
V
D
C_1 Residue
CTL Response (%)
100
75
50
25
0

FIG.5

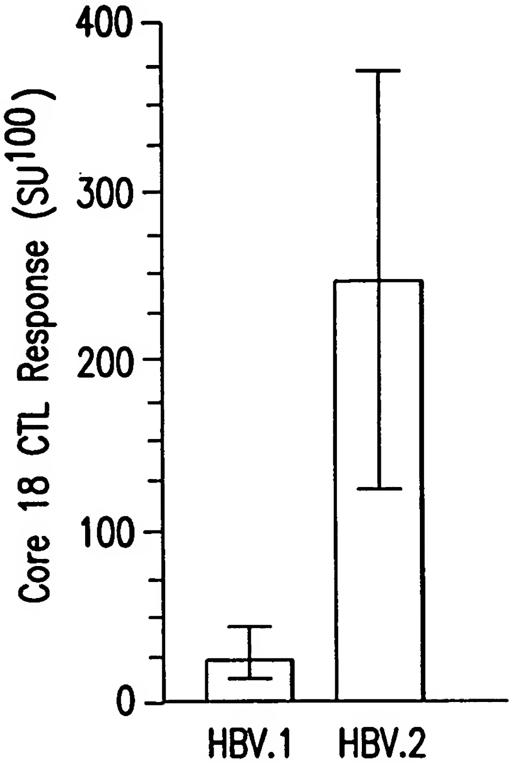
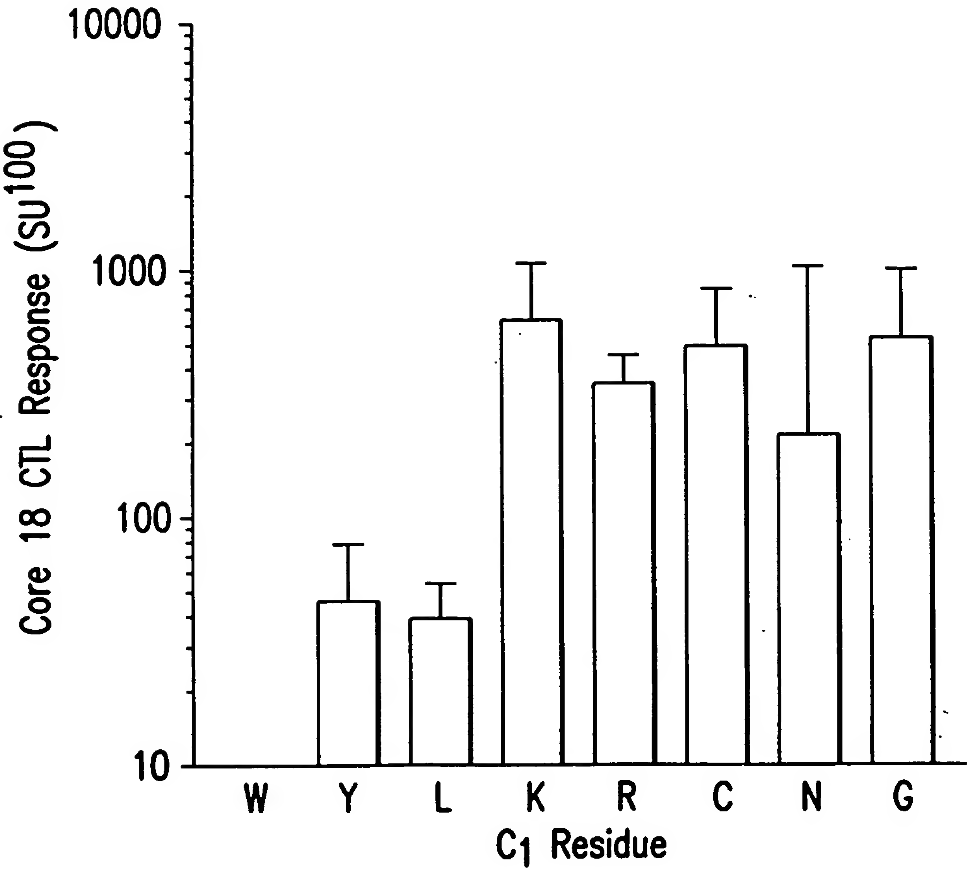

Core 18 CTL Response (SU100)
400
300
200
100
0
HBV.1
HBV.2

FIG.6A


Core 18 CTL Response (SU100)
10000
1000
100
10
W
Y
L
K
R
C
N
G
C1 Residue

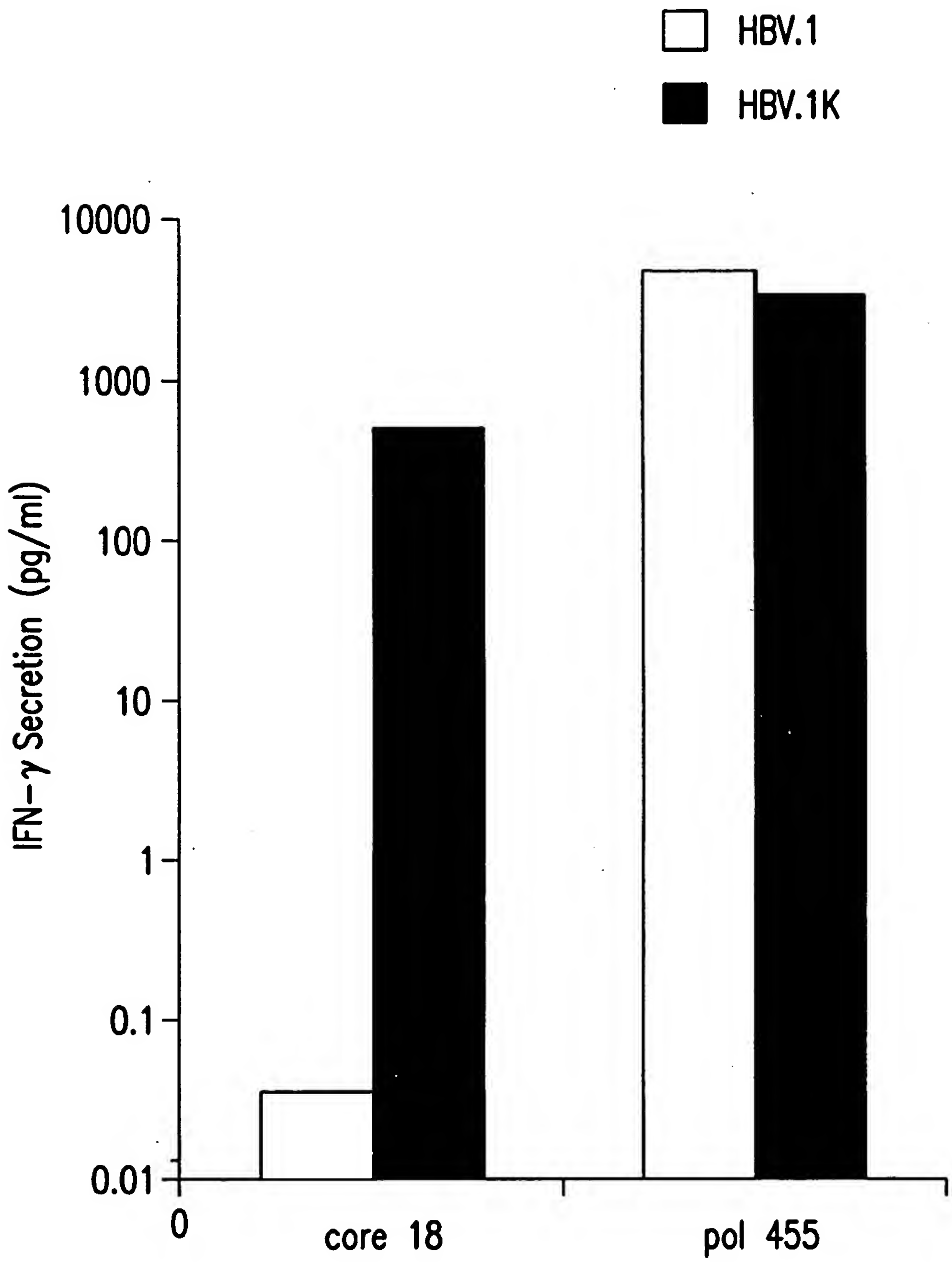
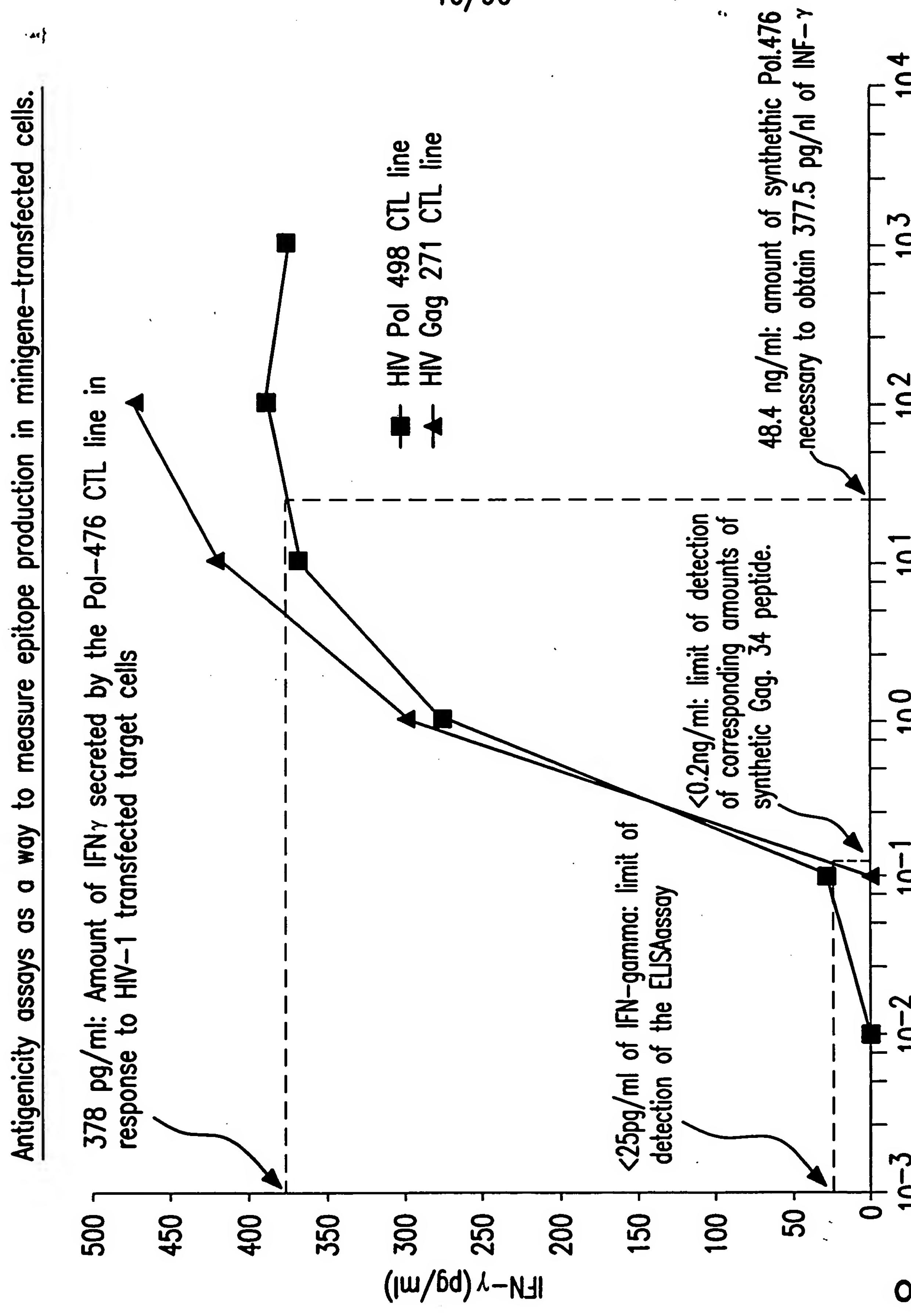

HBV.1
HBV.1K
10000
1000
100
10
1
0.1
0.01
0
IFN-γ Secretion (pg/ml)
core 18
pol 455

FIG.7


Antigenicity assays as a way to measure epitope production in minigene-transfected cells.
378 pg/ml: Amount of IFNγ secreted by the Pol-476 CTL line in response to HIV-1 transfected target cells
<25pg/ml of IFN-gamma: limit of detection of the ELISAassay
<0.2ng/ml: limit of detection of corresponding amounts of synthetic Gag. 34 peptide.
48.4 ng/ml: amount of synthethic Pol.476 necessary to obtain 377.5 pg/nl of INF-γ
HIV Pol 498 CTL line
HIV Gag 271 CTL line
IFN-γ (pg/ml)
500
450
400
350
300
250
200
150
100
50
0
10^{-3}
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}

G.8

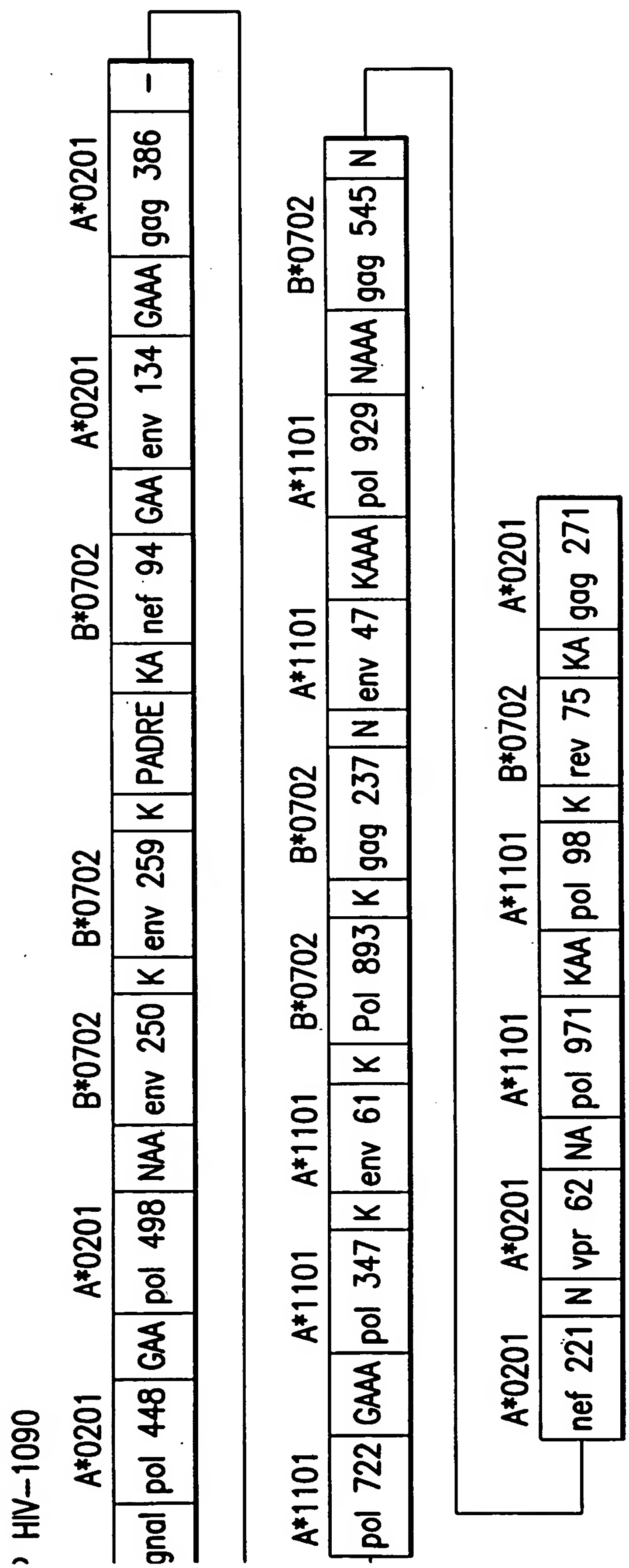

HIV-1090
gnal
A*0201
pol 448
GAA
A*0201
pol 498
NAA
B*0702
env 250
K
B*0702
env 259
K
PADRE
KA
B*0702
nef 94
GAA
A*0201
env 134
GAAA
A*0201
gag 386
I
A*1101
pol 722
GAAA
A*1101
pol 347
K
A*1101
env 61
K
B*0702
Pol 893
K
B*0702
gag 237
N
A*1101
env 47
KAAA
A*1101
pol 929
NAAA
B*0702
gag 545
N
A*0201
nef 221
N
A*0201
vpr 62
NA
A*1101
pol 971
KAA
A*1101
pol 98
K
B*0702
rev 75
KA
A*0201
gag 271

FIG.9A

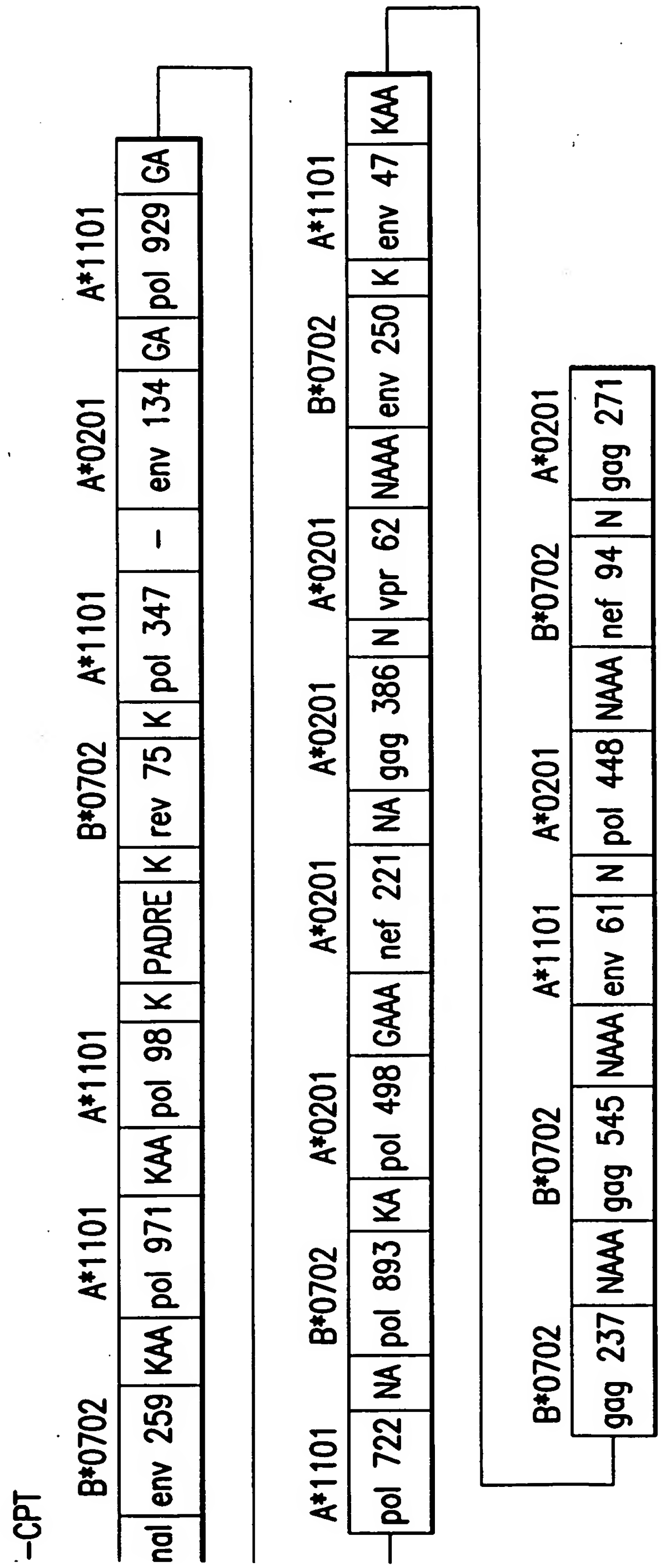

-CPT
B*0702
A*1101
A*1101
B*0702
A*1101
A*0201
A*1101
nal
env 259
KAA
pol 971
KAA
pol 98
K
PADRE
K
rev 75
K
pol 347
-
env 134
GA
pol 929
GA
A*1101
B*0702
A*0201
A*0201
A*0201
A*0201
B*0702
A*1101
pol 722
NA
pol 893
KA
pol 498
GAAA
nef 221
NA
gag 386
N
vpr 62
NAAA
env 250
K
env 47
KAA
B*0702
B*0702
A*1101
A*0201
B*0702
A*0201
gag 237
NAAA
gag 545
NAAA
env 61
N
pol 448
NAAA
nef 94
N
gag 271

FIG.9B

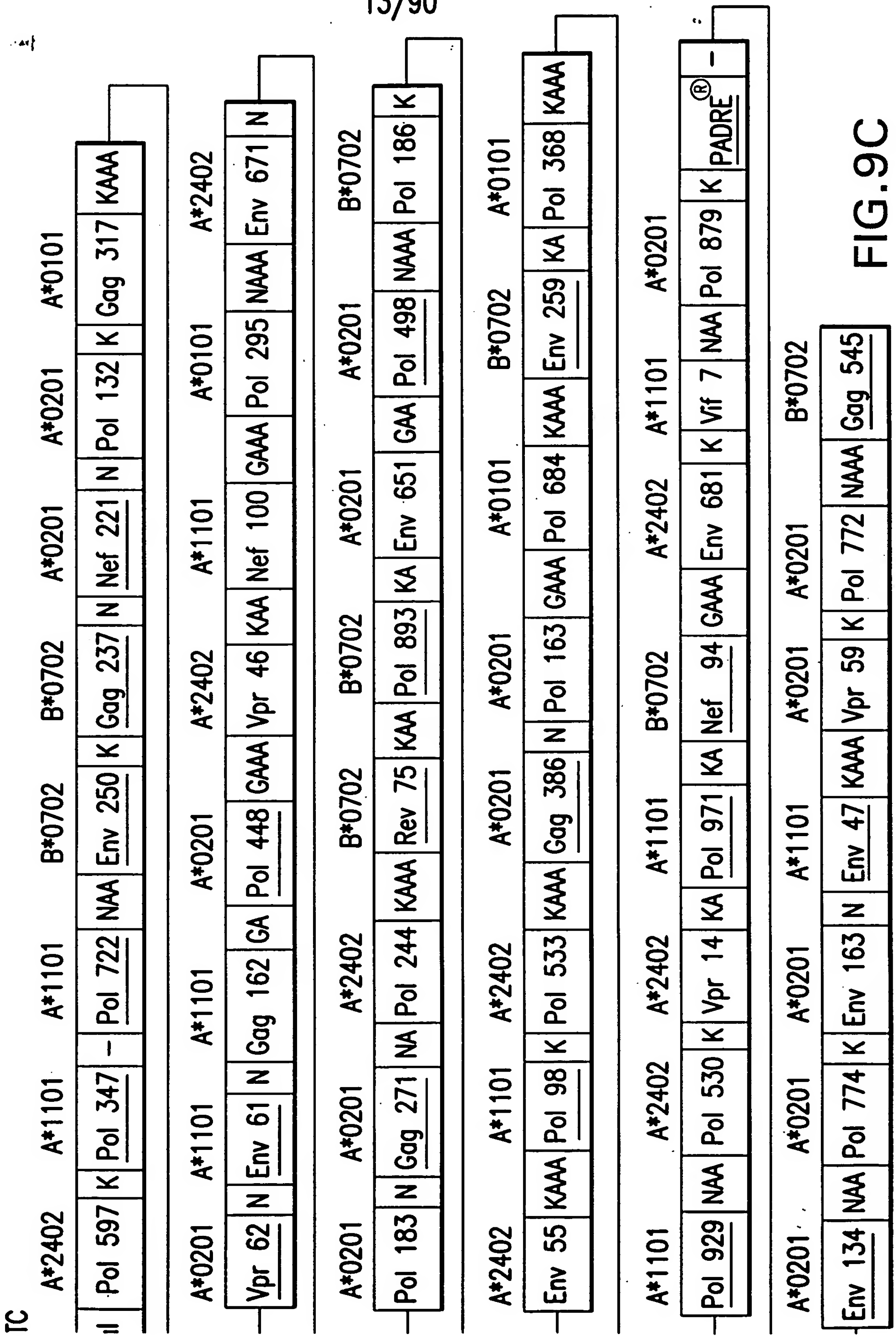

TC
A*2402 A*1101 A*1101 B*0702 B*0702 A*0201 A*0201 A*0101
Pol 597 | K | Pol 347 | – | Pol 722 | NAA | Env 250 | K | Gag 237 | N | Nef 221 | N | Pol 132 | K | Gag 317 | KAAA
A*0201 A*1101 A*1101 A*0201 A*2402 A*1101 A*0101 A*2402
Vpr 62 | N | Env 61 | N | Gag 162 | GA | Pol 448 | GAAA | Vpr 46 | KAA | Nef 100 | GAAA | Pol 295 | NAAA | Env 671 | N
A*0201 A*0201 A*2402 B*0702 B*0702 A*0201 A*0201 B*0702
Pol 183 | N | Gag 271 | NA | Pol 244 | KAAA | Rev 75 | KAA | Pol 893 | KA | Env 651 | GAA | Pol 498 | NAAA | Pol 186 | K
A*2402 A*1101 A*2402 A*0201 A*0201 A*0101 B*0702 A*0101
Env 55 | KAAA | Pol 98 | K | Pol 533 | KAAA | Gag 386 | N | Pol 163 | GAAA | Pol 684 | KAAA | Env 259 | KA | Pol 368 | KAAA
A*1101 A*2402 A*2402 A*1101 B*0702 A*2402 A*1101 A*0201
Pol 929 | NAA | Pol 530 | K | Vpr 14 | KA | Pol 971 | KA | Nef 94 | GAAA | Env 681 | K | Vif 7 | NAA | Pol 879 | K | PADRE® | –
A*0201 A*0201 A*0201 A*1101 A*0201 A*0201 B*0702
Env 134 | NAA | Pol 774 | K | Env 163 | N | Env 47 | KAAA | Vpr 59 | K | Pol 772 | NAAA | Gag 545

FIG.9C

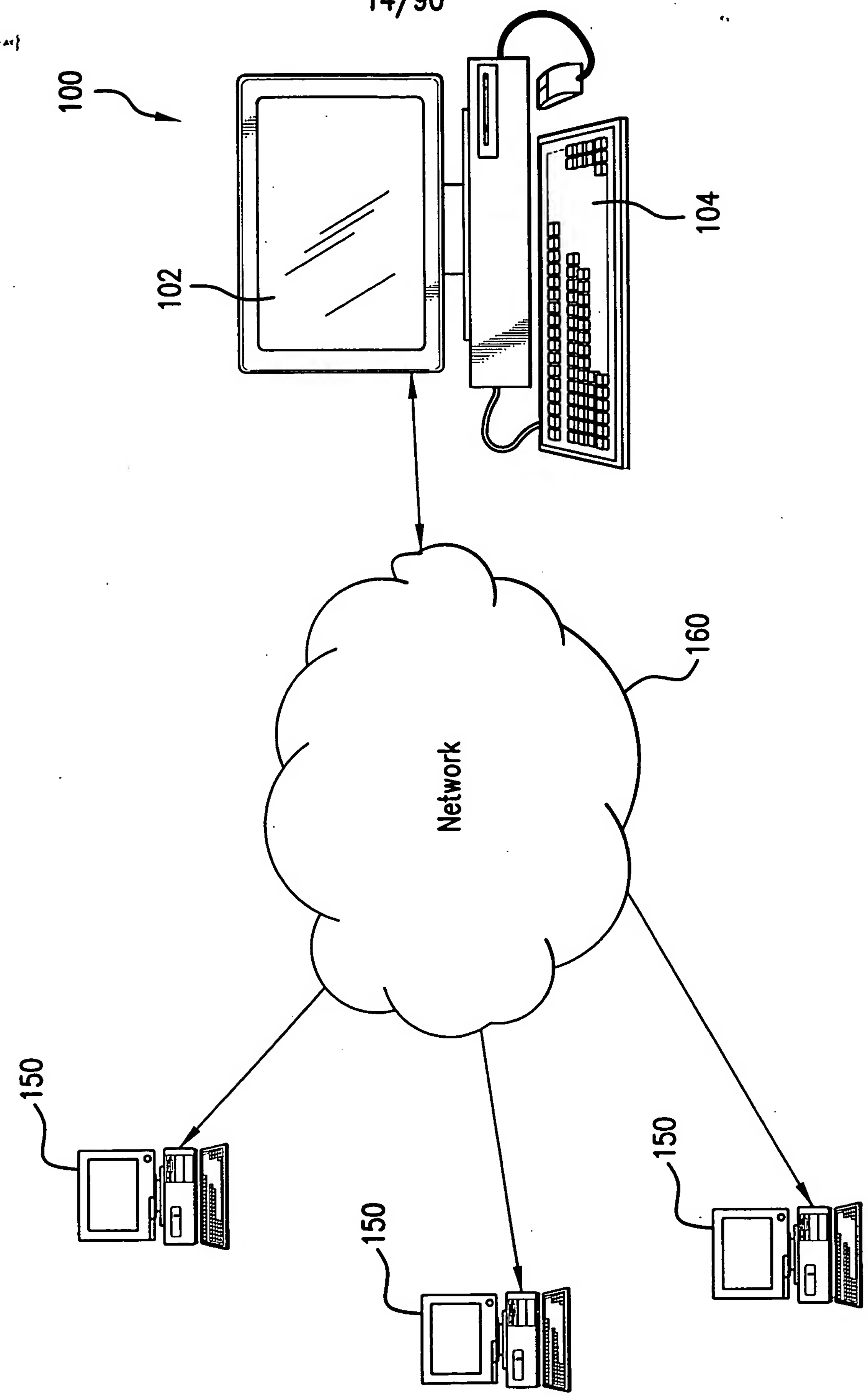


FIG.10

200

Sequence	Length	Code
VLAEAMSQV	9	A
ILKEPVHGV	9	B
TLNFPISPI	9	C
SLLNATDIAV	10	D
QMAVFIHNFK	10	E
VTVYYGVPVWK	11	F
FPVRPQVPL	9	G
YPLASLRSLF	10	H
VIYQYMDDLY	10	I
IYQEPFKNL	9	J
IWGCSGKLI	9	K

202

AA	C+1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

204

Motif Specification
XXXX(FY)XX(LIMV)
XXXX(FY)XXX(LIMV)
XXXXNXXX(LIMV)
XXXXNXXXX(LIMV)
X(LM)XXXXXXV
X(LM)XXXXXXXV
X(LMVT)XXXXXX(KRY)
X(LMVT)XXXXXXX(KRY)

206

MaxInsertions={enter value here} 208

OutputToScreen=yes/no 210

OutputToFile=yes/no 212

MinimumAccepted={enter value here} 214

MaxDuplicateFunctionValues={enter value here} 216

MaxSearchTime (min.)={enter value here} 218

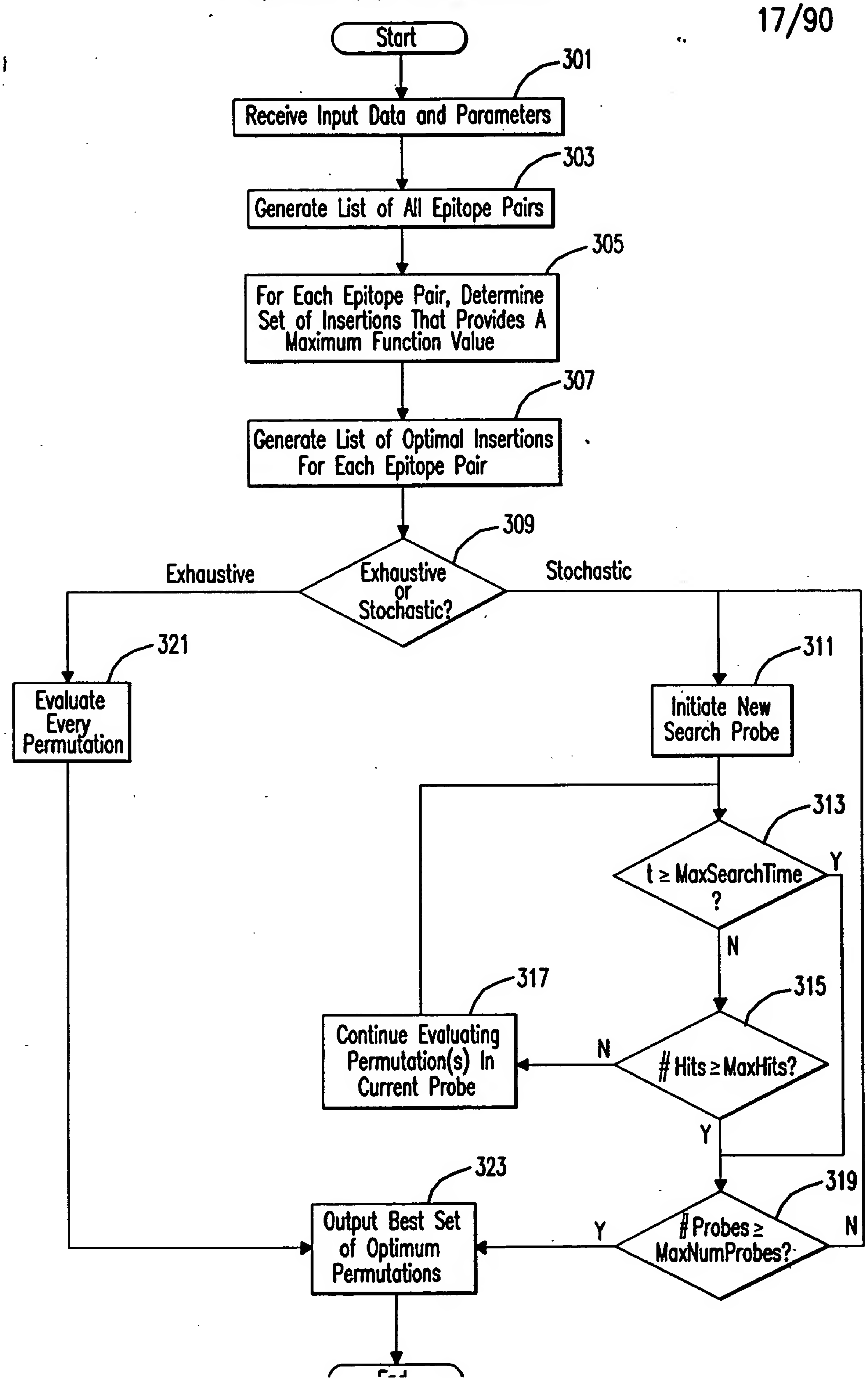
Exhaustive=yes/no 220

NumStochasticProbes={enter value here} 222

MaxHitsPerProbe={enter value here} 224

RandomProbeStart=yes/no 226

FIG.11B


Start
301
Receive Input Data and Parameters
303
Generate List of All Epitope Pairs
305
For Each Epitope Pair, Determine Set of Insertions That Provides A Maximum Function Value
307
Generate List of Optimal Insertions For Each Epitope Pair
309
Exhaustive or Stochastic?
Exhaustive
Stochastic
321
Evaluate Every Permutation
311
Initiate New Search Probe
313
t ≥ MaxSearchTime ?
Y
N
317
Continue Evaluating Permutation(s) In Current Probe
315
Hits ≥ MaxHits?
N
Y
323
Output Best Set of Optimum Permutations
319
Probes ≥ MaxNumProbes?
Y
N

Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

204

The following 10 motif specifications will be used to search for junctionals.

Count	Motif Specification
1	XXXX(FY)XX(LIMV)
2	XXXX(FY)XXX(LIMV)
3	XXXXNXXX(LIMV)
4	XXXXNXXXX(LIMV)
5	X(LM)XXXXXXV
6	X(LM)XXXXXXXV
7	X(LMVT)XXXXXX(KRY)
8	X(LMVT)XXXXXXX(KRY)
9	XPXXXXXX(LIMVF)
10	XPXXXXXXX(LIMVF)

206

Code	Peptide	Length
A	VLAEAMSQV	9
B	ILKEPVHGV	9
C	TLNFPISPI	9
D	SLLNATDIAV	10
E	QMAVFIHNFK	10
F	VTVYYGVPVWK	11
G	FPVRPQVPL	9
H	YPLASLRSLF	10
I	VIYQYMDDLY	10
J	IYQEPFKNL	9
K	IWGCSGKLI	9

202

}

OutputToScreen = No

OutputToFile = Yes

MinimumValueAccepted = 0

MaxDuplicateFunctionValues = 50

SearchTime = 5

NumStochasticProbes = 10

MaxHitsPerProbe = 25

RandomProbeStart = Yes

Col. 1 Code 1	Col. 2 I1	Col. 3 I2	Col. 4 I3	Col. 5 I4	Col. 6 Code 2	Col. 7 C	Col. 8 N	Col. 9 C+N	Col. 10 J	Col. 11 MaxFunc.
A	C	A		L	B	2.00	2.20	4.40	0	8.80
A	C			L	C	2.00	2.20	4.40	0	8.80
A	C			L	D	2.00	2.20	4.40	0	8.80
A	C			L	E	2.00	2.20	4.40	0	8.80
A	C			R	F	2.00	1.57	3.14	2	1.57
A	C			R	G	2.00	1.57	3.14	1	3.14
A	C			R	H	2.00	1.57	3.14	0	6.28
A	G				I	1.80	1.33	2.39	1	2.39
A	C	A	A	G	J	2.00	1.33	2.66	0	5.32
A	C			R	K	2.00	1.57	3.14	0	6.28
B	C	A	A	G	A	2.00	1.33	2.66	0	5.32
B	C	A		R	C	2.00	1.57	3.14	0	6.28
B	C	A		R	D	2.00	1.57	3.14	0	6.28
B	C	A		R	E	2.00	1.57	3.14	0	6.28
B	C	A	A	G	F	2.00	1.33	2.66	1	2.66
B	C			R	G	2.00	1.57	3.14	1	3.14
B	C			R	H	2.00	1.57	3.14	0	6.28
B	C	A	A	G	I	2.00	1.33	2.66	1	2.66
B	C	A	A	G	J	2.00	1.33	2.66	0	5.32
B	C	A	A	G	K	2.00	1.33	2.66	0	5.32
C	C	A		R	A	2.00	1.57	3.14	1	3.14
C	C	A		R	B	2.00	1.57	3.14	1	3.14
C	C			L	D	2.00	2.20	4.40	1	4.40
C	C	A		R	E	2.00	1.57	3.14	1	3.14
C	C			R	F	2.00	1.57	3.14	1	3.14
C	C			R	G	2.00	1.57	3.14	1	3.14
C	C			R	H	2.00	1.57	3.14	0	6.28
C	C	A		R	I	2.00	1.57	3.14	1	3.14
C	C	A	A	R	J	2.00	1.57	3.14	0	6.28
C	C	A	A	R	K	2.00	1.57	3.14	0	6.28

FIG. 13B

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
D	C			L	A	2.00	2.20	4.40	0	8.80
D	C			L	B	2.00	2.20	4.40	0	8.80
D	C			L	C	2.00	2.20	4.40	0	8.80
D	C			L	E	2.00	2.20	4.40	0	8.80
D	G				F	1.80	1.33	2.39	0	4.79
D	C			R	G	2.00	1.57	3.14	0	6.28
D	C	A	A	G	H	2.00	1.33	2.66	0	5.32
D	C			L	I	2.00	2.20	4.40	1	4.40
D	C	A		G	J	2.00	1.33	2.66	0	5.32
D	C			R	K	2.00	1.57	3.14	0	6.28
E	C	A	A	L	A	2.00	2.20	4.40	0	8.80
E	C	A	A	L	B	2.00	2.20	4.40	0	8.80
E	C	A	A	L	C	2.00	2.20	4.40	0	8.80
E	C	A	A	L	D	2.00	2.20	4.40	0	8.80
E	C	A		R	F	2.00	1.57	3.14	0	6.28
E	C	A		R	G	2.00	1.57	3.14	0	6.28
E	C	A		R	H	2.00	1.57	3.14	0	6.28
E	C	A	A	L	I	2.00	2.20	4.40	0	8.80
E	C	A		R	J	2.00	1.57	3.14	0	6.28
E	C	A		R	K	2.00	1.57	3.14	0	6.28
F	K			L	A	2.20	2.20	4.84	1	4.84
F	K	A	A	G	B	2.20	1.33	2.93	1	2.93
F	K	A	A	G	C	2.20	1.33	2.93	0	5.85
F	K	A	A	G	D	2.20	1.33	2.93	0	5.85
F	K	A	A	G	E	2.20	1.33	2.93	0	5.85
F	K	A		G	G	2.20	1.33	2.93	1	2.93
F	K	A		G	H	2.20	1.33	2.93	1	2.93
F	K	A	A	G	I	2.20	1.33	2.93	1	2.93
F	K			R	J	2.20	1.57	3.45	1	3.45
F	K			R	K	2.20	1.57	3.45	0	6.91
G	C	A		R	A	2.00	1.57	3.14	1	3.14
G	C	A		R	B	2.00	1.57	3.14	2	1.57
G	C	A		R	C	2.00	1.57	3.14	1	3.14
G	C			L	D	2.00	2.20	4.40	1	4.40
G	C	A		R	E	2.00	1.57	3.14	2	1.57
G	C			L	F	2.00	2.20	4.40	4	1.10
G	C			G	H	2.00	1.33	2.66	0	5.32
G	C	A	A	R	I	2.00	1.57	3.14	2	1.57
G	C	A	A	R	J	2.00	1.57	3.14	1	3.14
G	C	A	A	R	K	2.00	1.57	3.14	0	6.28
H	C	A	A	G	A	2.00	1.33	2.66	0	5.32
H	C	A	A	G	B	2.00	1.33	2.66	1	2.66
H	C	A		G	C	2.00	1.33	2.66	0	5.32
H	C	A		G	D	2.00	1.33	2.66	0	5.32
H	C	A	A	G	E	2.00	1.33	2.66	0	5.32
H	C	A	A	G	F	2.00	1.33	2.66	1	2.66
H	C			R	G	2.00	1.57	3.14	1	3.14
H	C	A	A	G	I	2.00	1.33	2.66	1	2.66
H	C	A		G	J	2.00	1.33	2.66	1	2.66
H	C	A	A	G	K	2.00	1.33	2.66	0	5.32

FIG.13C

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
I	K	A	A	G	A	2.20	1.33	2.93	0	5.85
I	K	A	A	G	B	2.20	1.33	2.93	1	2.93
I	K	A		G	C	2.20	1.33	2.93	0	5.85
I	K	A		G	D	2.20	1.33	2.93	0	5.85
I	K	A	A	G	E	2.20	1.33	2.93	0	5.85
I	K	A	A	G	F	2.20	1.33	2.93	1	2.93
I	K			R	G	2.20	1.57	3.45	1	3.45
I	K	A	A	G	H	2.20	1.33	2.93	0	5.85
I	K	A		G	J	2.20	1.33	2.93	1	2.93
I	K	A	A	G	K	2.20	1.33	2.93	0	5.85
J	K	A	A	R	A	2.20	1.57	3.45	0	6.91
J	K	A	A	R	B	2.20	1.57	3.45	1	3.45
J	K	A		R	C	2.20	1.57	3.45	0	6.91
J	K	A		R	D	2.20	1.57	3.45	0	6.91
J	K	A		R	E	2.20	1.57	3.45	1	3.45
J	K	A	A	R	F	2.20	1.57	3.45	2	1.73
J	K			R	G	2.20	1.57	3.45	1	3.45
J	K			R	H	2.20	1.57	3.45	0	6.91
J	K	A	A	R	I	2.20	1.57	3.45	1	3.45
J	K	A	A	R	K	2.20	1.57	3.45	0	6.91
K	K			L	A	2.20	2.20	4.84	0	9.68
K	K			L	B	2.20	2.20	4.84	0	9.68
K	K			L	C	2.20	2.20	4.84	0	9.68
K	K			L	D	2.20	2.20	4.84	0	9.68
K	K	A	A	L	E	2.20	2.20	4.84	0	9.68
K	K	A	A	R	F	2.20	1.57	3.45	1	3.45
K	G				G	1.80	1.33	2.39	0	4.79
K	K			R	H	2.20	1.57	3.45	0	6.91
K	K			L	I	2.20	2.20	4.84	1	4.84
K	K			R	J	2.20	1.57	3.45	0	6.91

Junctional Analyzer took 142.77 seconds.

FIG. 13D

Appl. No. 10/677,754; Filed: Oct 3, 2003
Dkt No. 2060.0200003/HCC/PAC; Group Unit: To be assigned
Inventors: SETTE et al.
Tel. No.: 202-371-2600
For: Optimized Multi-Epitope Constructs and Uses Thereof

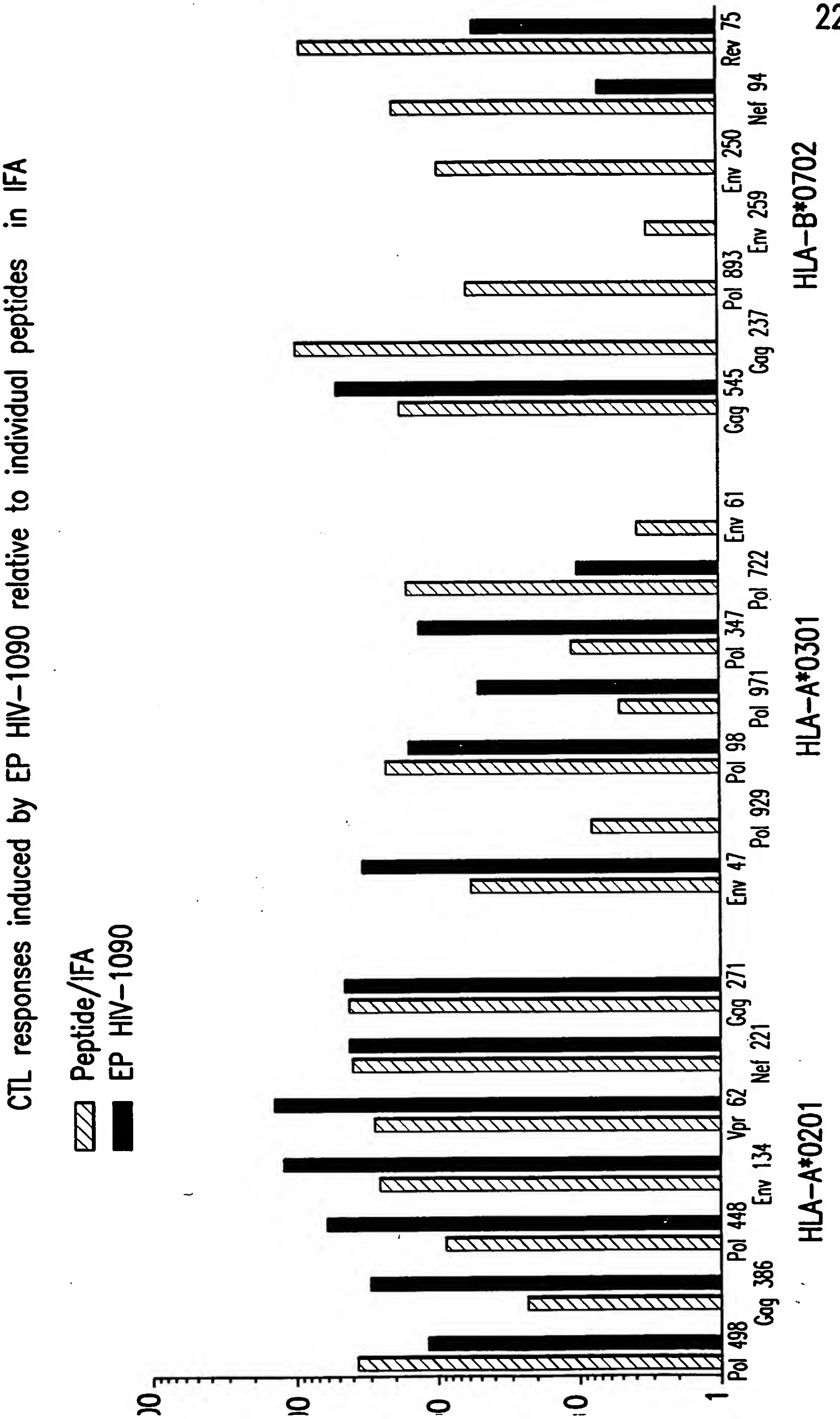


FIG.14A

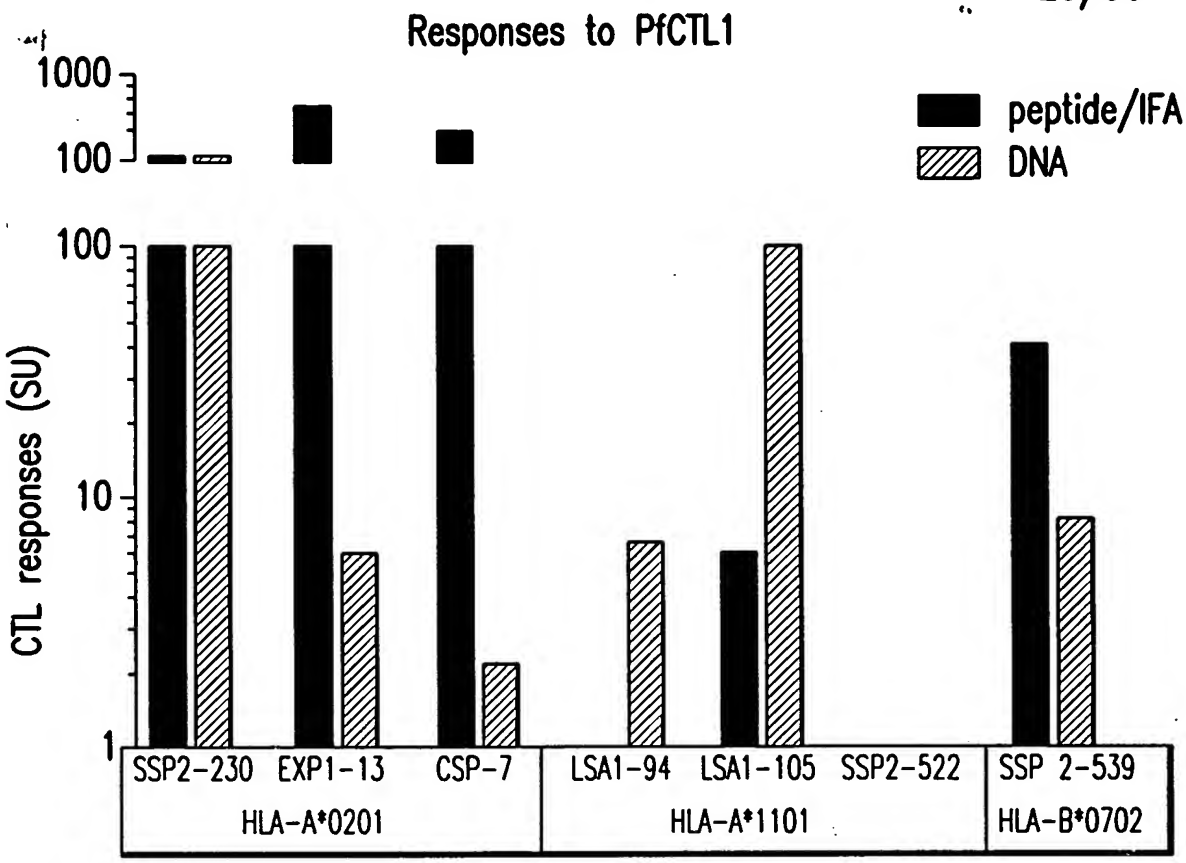
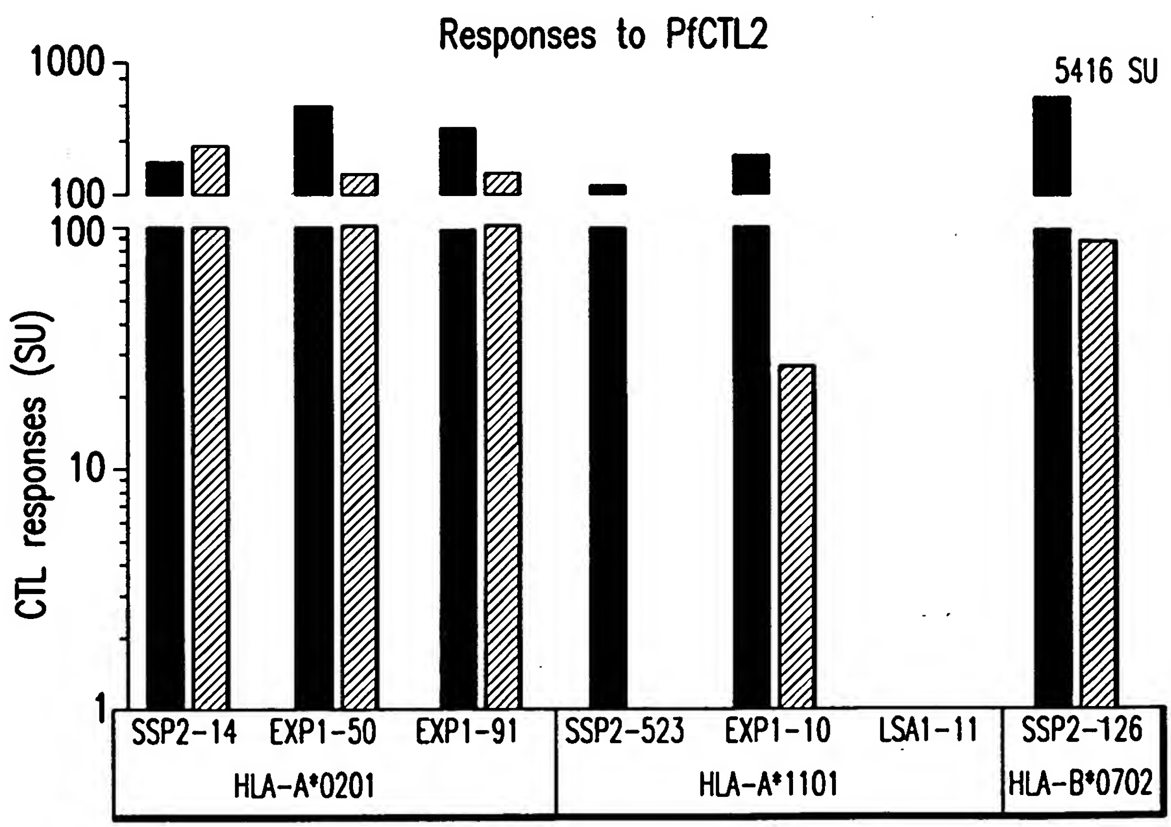

Responses to PfCTL1
1000
100
100
10
1
CTL responses (SU)
peptide/IFA
DNA
SSP2-230
EXP1-13
CSP-7
LSA1-94
LSA1-105
SSP2-522
SSP 2-539
HLA-A*0201
HLA-A*1101
HLA-B*0702

FIG.14B-1


Responses to PfCTL2
5416 SU
1000
100
100
10
1
CTL responses (SU)
SSP2-14
EXP1-50
EXP1-91
SSP2-523
EXP1-10
LSA1-11
SSP2-126
HLA-A*0201
HLA-A*1101
HLA-B*0702

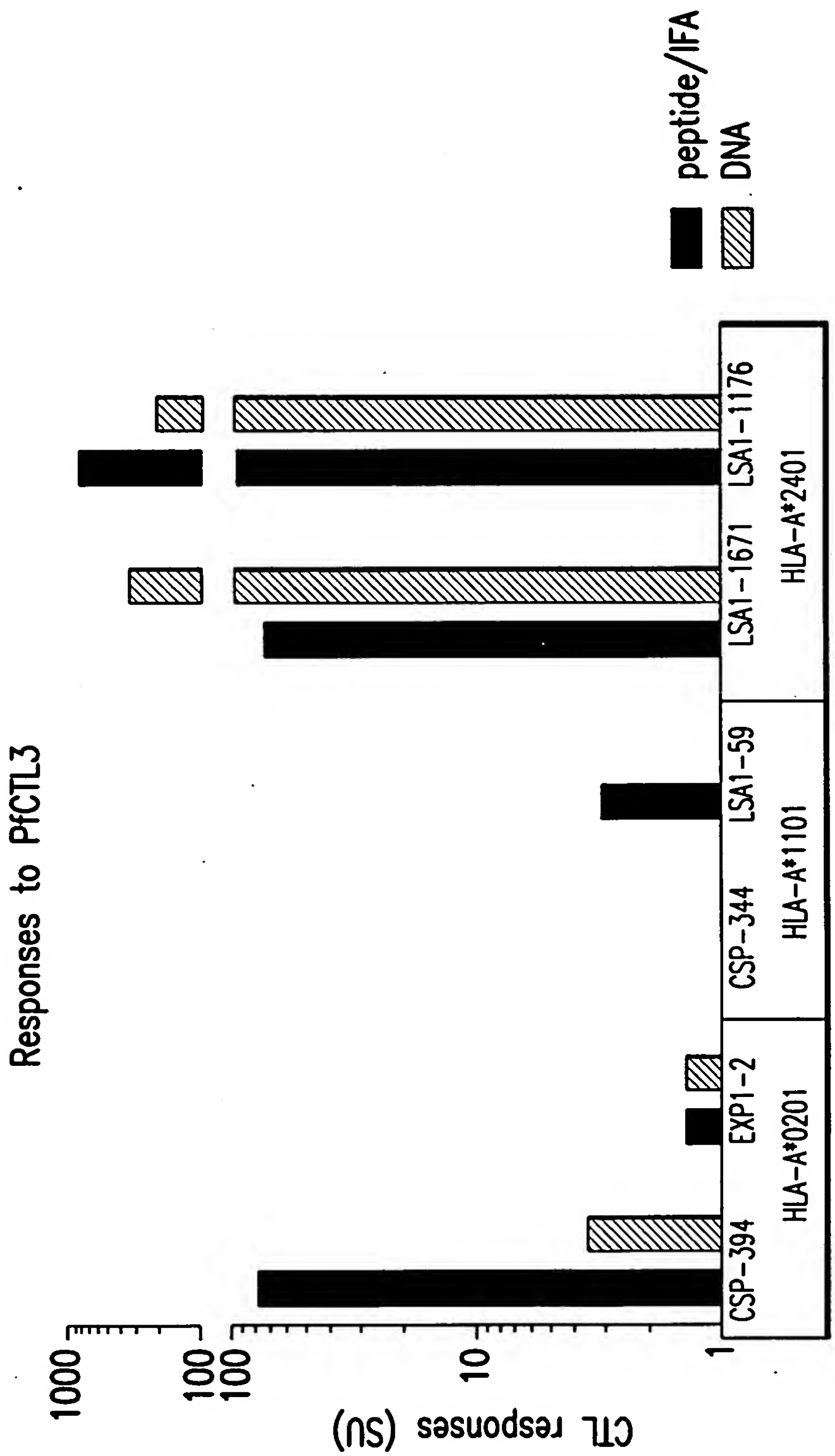

Responses to PfCTL3
peptide/IFA
DNA
CTL responses (SU)
1000
100
100
10
1
CSP-394
EXP1-2
HLA-A*0201
CSP-344
LSA1-59
HLA-A*1101
LSA1-1671
LSA1-1176
HLA-A*2401

FIG.14B-3

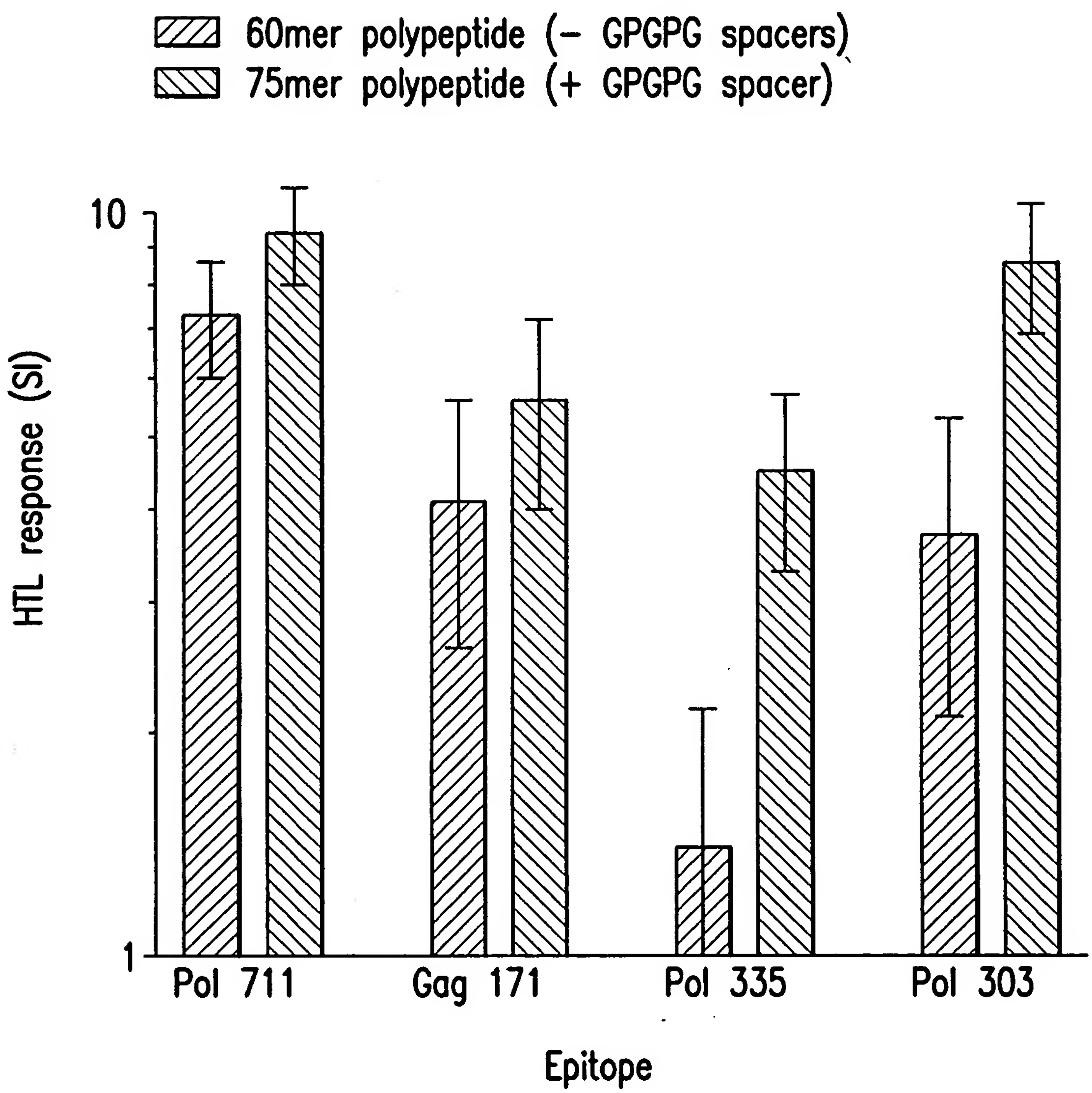

60mer polypeptide (– GPGPG spacers)
75mer polypeptide (+ GPGPG spacer)
10
1
HTL response (SI)
Pol 711
Gag 171
Pol 335
Pol 303
Epitope

FIG.15

Appl. No. 10/677,754; Filed: Oct 3, 2003
Dkt No. 2060.0200003/HCC/PAC; Group Unit: To be assigned
Inventors: SETTE et al.
Tel. No.: 202-371-2600
For: Optimized Multi-Epitope Constructs and Uses Thereof

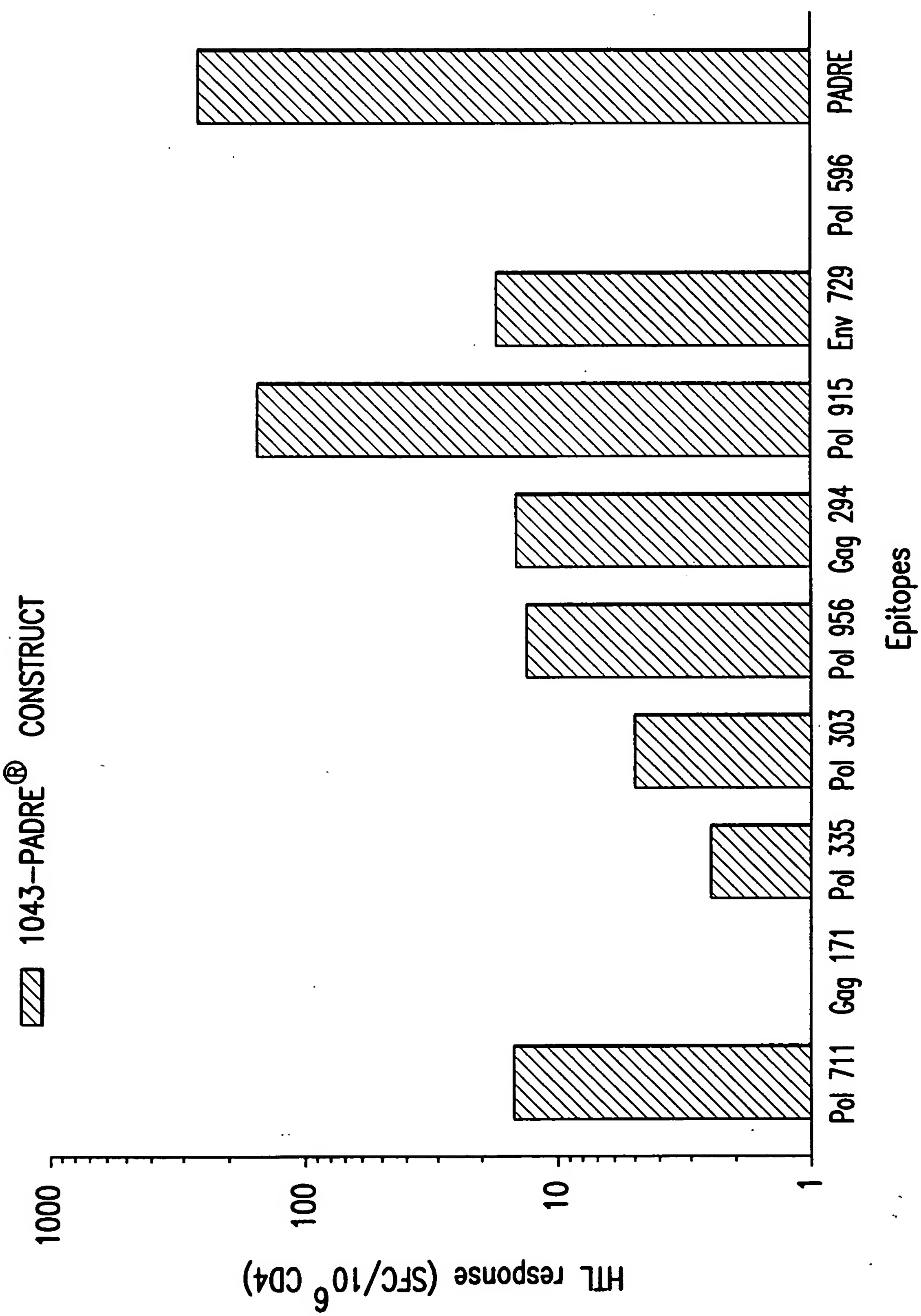


FIG.16

Appl. No. 10/677,754; Filed: Oct 3, 2003
Dkt No. 2060.0200003/HCC/PAC; Group Unit: To be assigned
Inventors: SETTE et al.
Tel. No.: 202-371-2600
For: Optimized Multi-Epitope Constructs and Uses Thereof

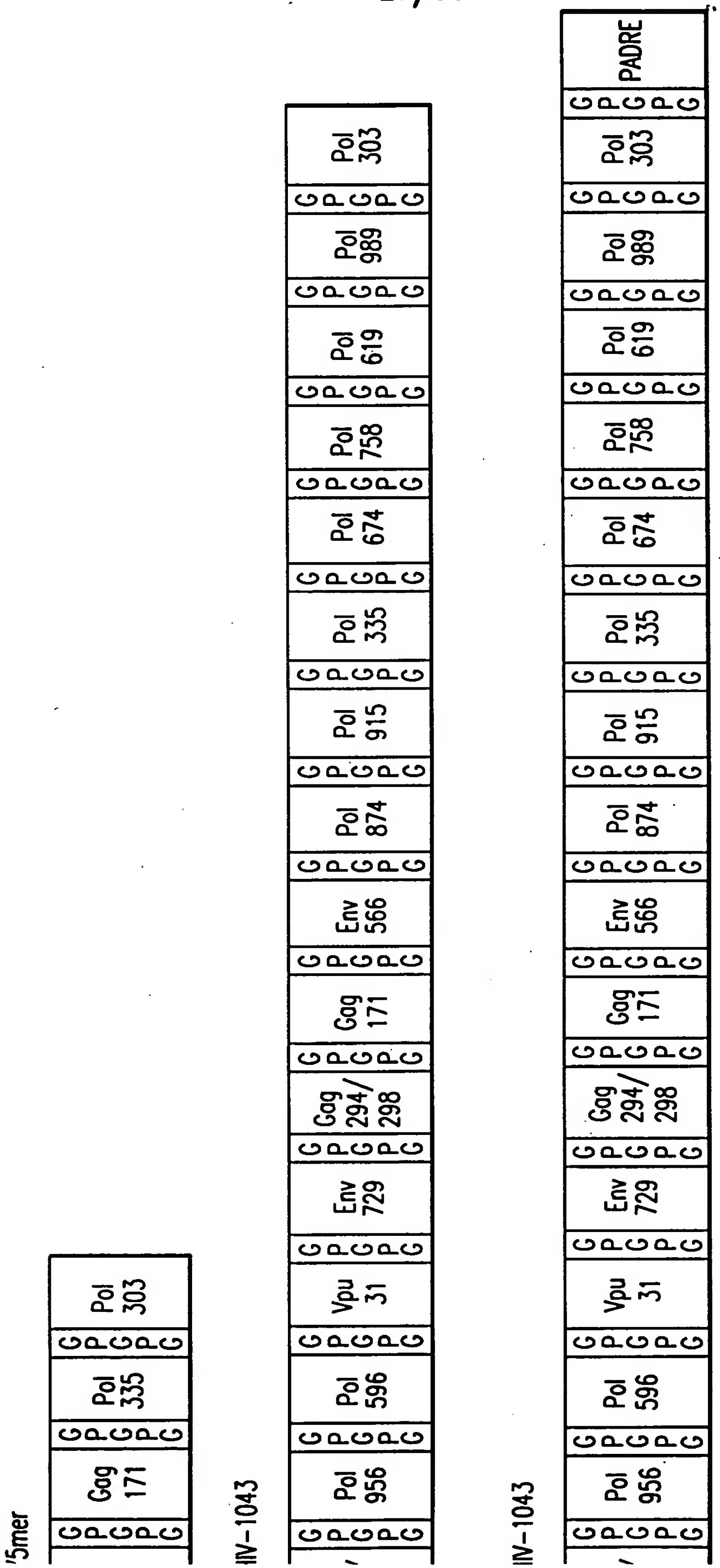


FIG.17

EP-HIV-1090

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPIKIPIHYCAPAKAKFVAAW
TLKAAAKAFPVRPQVPLGAAKLTPLCVTLGAAAVLAEAMSQVKVYLAWVPAHKGAAAAIFQSSMTKKTTLFCA
SDAKNIPYNPQSQGVVKHPVHAGPIANVTVYYGVPVWKKAAAQMAVFIHNFKNAAAYPLASLRSLFNLTFGWC
FKLNRILQQLLFINAKIQNFRVYYRKAAVTIKIGGQLKKVPLQLPPLKAMTNNPPIPV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAAGCTGG
TGGGCAAACTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGGGGTGAATGCCGCTTGCCCTAA
AGTCAGCTTCGAACCAATTAAGATCCCCATTCATTACTGTGCACCTGCCAAAGCTAAGTTTGTGGCCGCTTGG
ACCCTCAAGGCCGCTGCAAAAGCCTTCCCAGTGAGGCCCCAGGTGCCTCTGGGCGCCGCTAAACTCACACCAC
TGTGCGTCACTCTGGGAGCCGCTGCAGTGCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGT
GCCCGCCCACAAGGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAACAACTCTGTTCTGTGCC
TCCGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGCCGGACCTA
TTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACAGATGGCCGTGTTTATTCA
CAATTTCAAAAACGCCGCTGCATACCCCCTCGCCAGCCTGAGATCCCTCTTCAACCTGACATTCGGCTGGTGC
TTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTTTATCAATGCTAAAATCCAGAACTTCCGCGTCTACTATA
GGAAGGCTGCAGTGACTATCAAAATTGGCGGACAACTGAAGAAAGTGCCTCTCCAGCTGCCCCCTCTCAAGGC
AATGACCAACAATCCCCCTATCCCAGTCTGA

HIV-CPT

MGMQVQIQSLFLLLLWVPGSRGIPIHYCAPAKAAKIQNFRVYYRKAAVTIKIGGQLKKAKFVAAWTLKAAAKV
PLQLPPLKAIFQSSMTKKLTPLCVTLGAQMAVFIHNFKGAKVYLAWVPAHKNAIPYNPQSQGVVKAILKEPVH
GVGAAALTFGWCFKLNAVLAEAMSQVNRILQQLLFINAAACPKVSFEPIKVTVYYGVPVWKKAAHPVHAGPIA
NAAAYPLASLRSLFNAAATTLFCASDAKNKLVGKLNWANAAAFPVRPQVPLNMTNNPPIPV

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAATCCCCA
TTCACTACTGCGCCCCTGCTAAGGCAGCCAAAATCCAGAACTTCAGGGTGTATTACAGAAAGGCTGCAGTCAC
CATTAAAATCGGCGGACAACTGAAGAAAGCCAAGTTTGTGGCCGCTTGGACACTCAAGGCCGCTGCAAAGGTC
CCACTGCAGCTCCCCCCTCTGAAGGCCATCTTCCAGAGCTCCATGACTAAGAAACTGACCCCACTGTGTGTGA
CACTCGGGGCCCAGATGGCTGTGTTCATCCATAATTTTAAAGGCGCCAAGGTCTACCTGGCTTGGGTGCCCGC
ACACAAGAACGCCATTCCTTACAATCCACAGTCTCAAGGAGTGGTCAAAGCTATTCTGAAGGAGCCCGTGCAC
GGGGTGGGCGCCGCTGCACTCACTTTCGGATGGTGCTTTAAACTGAACGCCGTGCTGGCTGAAGCCATGAGCC
AGGTCAATCGGATCCTGCAGCAACTGCTCTTCATTAACGCCGCTGCATGTCCTAAGGTGTCCTTCGAGCCAAT
CAAAGTGACCGTGTATTACGGGGTCCCCGTGTGGAAGAAAGCCGCTCATCCTGTCCACGCAGGCCCAATCGCC
AACGCCGCTGCATATCCCCTCGCCTCTCTGCGCAGCCTGTTTAACGCCGCTGCAACAACCCTCTTTTGCGCCT
CCGACGCTAAGAATAAACTGGTGGGAAAGCTGAACTGGGCCAACGCAGCTGCATTCCCTGTGAGGCCACAGGT
CCCCCTCAATATGACTAACAATCCCCCTATCCCAGTGTGA

FIG.18A

HIV-FT

MQVQIQSLFLLLLWVPGSRGKLVGKLNWAMASDFNLPPVAIFQSSMTKVTIKIGGQLKRILQQLLFIMAVFIH
NFKIPYNPQSQGVVTTLFCASDAKILKEPVHGVQMAVFIHNFKGAAVFIHNFKRCPKVSFEPIKIQNFRVYYR
LTFGWCFKLQVPLRPMTYKMTNNPPIPVTVYYGVPVWKVLAEAMSQVIPIHYCAPAKLTPLCVTL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAAGCTGGTGGGGA
AGCTGAACTGGGCCATGGCCAGCGATTTCAACCTGCCCCCCGTGGCCATCTTCCAGAGCAGCATGACCAAGGT
GACCATCAAGATCGGGGGGCAGCTGAAGAGGATCCTGCAGCAGCTGCTGTTCATCATGGCCGTGTTCATCCAC
AACTTCAAGATCCCCTACAACCCCCAGAGCCAGGGGGTGGTGACCACCCTGTTCTGCGCCAGCGATGCCAAGA
TCCTGAAGGAGCCCGTGCACGGGGTGCAGATGGCCGTGTTCATCCACAACTTCAAGGGCGCCGCCGTGTTCAT
CCACAACTTCAAGAGGTGCCCCAAGGTGAGCTTCGAGCCCATCAAGATCCAGAACTTCAGGGTGTACTACAGG
CTGACCTTCGGGTGGTGCTTCAAGCTGCAGGTGCCCCTGAGGCCCATGACCTACAAGATGACCAACAACCCCC
CCATCCCCGTGACCGTGTACTACGGGGTGCCCGTGTGGAAGGTGCTGGCCGAGGCCATGAGCCAGGTGATCCC
CATCCACTACTGCGCCCCCGCCAAGCTGACCCCCCTGTGCGTGACCCTG

FIG.18B

HIV-TC

MGMQVQIQSLFLLLLWVPGSRGYWQATWIPEWKAIFQSSMTKKVYLAWVPAHKNAACPKVSFEPIKHPVHAGP
IANLTFGWCFKLNKMIGGIGGFIKFRDYVDRFYKAAARILQQLLFINTTLFCASDAKNQMVHQAISPRGAKLV
GKLNWAGAAAIYETYGDTWKAAQVPLRPMTYKGAAAVTVLDVGDAYNAAARYLKDQQLLNTLNFPISPINMTN
NPPIPVNAPYNTPVFAIKAAAVPLQLPPLKAAIPYNPQSQGVVKALLQLTVWGIGAAILKEPVHGVNAAAFPI
SPIETVKVWKEATTTLFKAAAVTIKIGGQLKKIYQEPFKNLKAAAVLAEAMSQVNLVGPTPVNIGAAAEVNIV
TDSQYKAAAIPIHYCAPAKAVIYQYMDDLYKAAAQMAVFIHNFKNAATYQIYQEPFKPYNEWTLELKAKIQNF
RVYYRKAFPVRPQVPLGAAAIWGCSGKLIKVMIVWQVDRNAAKAACWWAGIKAKFVAAWTLKAAAKLTPLCVT
LNAAMASDFNLPPVKSLLNATDIAVNVTVYYGVPVWKKAAAAIIRILQQLKRAMASDFNLNAAAYPLASLRSL
F

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCTAGAGGATACTGGC
AAGCTACTTGGATTCCAGAATGGAAAGCTATCTTTCAATCCTCAATGACGAAGAAGGTATACCTGGCATGGGT
CCCAGCACACAAGAACGCCGCTTGCCCAAAGGTGTCCTTTGAACCCATTAAACACCCAGTGCACGCAGGGCCA
ATAGCGAATTTGACATTCGGGTGGTGCTTCAAACTAAACAAAATGATCGGCGGCATTGGAGGCTTTATCAAGT
TTAGAGATTACGTGGACCGATTCTATAAAGCCGCTGCCCGTATACTCCAGCAGCTACTATTCATCAACACCAC
TCTCTTCTGCGCTTCAGACGCTAAGAACCAAATGGTACACCAAGCCATAAGCCCTAGAGGAGCCAAGCTCGTA
GGGAAATTAAATTGGGCGGGTGCAGCAGCAATCTACGAGACTTACGGCGATACCTGGAAAGCAGCCCAGGTTC
CGTTACGCCCAATGACCTATAAAGGCGCAGCAGCAGTAACAGTTCTAGATGTAGGAGACGCTTACAACGCTGC
CGCAAGATACCTAAAAGATCAGCAGTTACTCAACACACTAAATTTCCCAATTAGCCCGATAAACATGACAAAT
AACCCACCAATTCCCGTCAATGCTCCCTACAACACTCCAGTATTCGCAATCAAAGCCGCTGCTGTCCCCCTGC
AGCTCCCTCCTCTGAAAGCTGCGATACCTTACAACCCACAGAGCCAAGGTGTTGTCAAAGCACTGCTTCAGCT
AACAGTTTGGGGAATTGGTGCTGCAATTCTAAAAGAGCCAGTTCATGGGGTTAACGCCGCCGCCTTCCCAATC
AGTCCTATTGAGACTGTGAAAGTATGGAAAGAAGCCACAACCACACTTTTTAAGGCAGCCGCAGTTACAATTA
AAATAGGGGGCCAACTTAAGAAAATATACCAGGAACCTTTCAAGAATCTCAAAGCCGCTGCAGTGCTCGCCGA
GGCTATGTCACAGGTGAATTTGGTCGGACCAACACCCGTAAACATCGGAGCCGCAGCCGAAGTGAACATAGTC
ACCGACTCACAGTACAAAGCCGCTGCAATACCCATACATTATTGTGCTCCCGCAAAGGCCGTGATCTATCAAT
ATATGGACGACCTGTATAAGGCCGCCGCGCAGATGGCAGTCTTTATCCACAACTTTAAAAACGCAGCTACTTA
TCAGATCTACCAGGAACCATTCAAACCGTACAATGAGTGGACCTTGGAACTAAAGGCCAAAATTCAGAACTTC
AGGGTATATTATAGAAAAGCATTTCCAGTGAGGCCCCAGGTGCCTCTGGGTGCCGCAGCAATATGGGGATGTT
CTGGAAAACTGATCAAGGTGATGATTGTATGGCAAGTGGACAGAAATGCAGCTAAGGCAGCCTGTTGGTGGGC
AGGTATAAAAGCAAAGTTCGTGGCAGCATGGACGCTTAAAGCAGCCGCAAAACTCACTCCTCTCTGCGTGACA
CTTAATGCAGCCATGGCCTCTGATTTCAACCTTCCCCCTGTAAAATCCCTGCTTAATGCGACAGATATCGCAG
TCAACGTAACAGTATATTATGGCGTGCCAGTCTGGAAAAAAGCCGCCGCGGCCATAATTCGGATACTGCAGCA
GCTGAAAAGAGCTATGGCGAGTGACTTCAACCTGAATGCGGCCGCCTACCCCTTGGCATCGTTAAGGTCACTA
TTTTGA

FIG.18C

HCV.1

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVDLMGYIPLVYLVAYQATVILAGYGAGVRLIVFPDLGVHMWNFISGI
YLLPRRGPRLYLVTRHADVVLVGGVLAALLFLLLADAFLLLADARVWMNRLIAFACTCGSSDLYLSAFSLHSYGVAGA
LVAFKLPGCSFSIFKTSERSQPRLIFCHSKKKFWAKHMWNFIPFYGKAIRMYVGGVEHRQLFTFSPRRRLGVRATRKV
GIYLLPNRAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGACTG
CTGTTCAACATCCTGGGGGGGTGGGTGGATCTGATGGGGTACATCCCCCTGGTGTACCTGGTGGCCTACCAGGCCACC
GTGATCCTGGCCGGGTACGGGGCCGGGGTGAGGCTGATCGTGTTCCCCGATCTGGGGGTGCACATGTGGAACTTCATC
AGCGGGATCTACCTGCTGCCCAGGAGAGGACCTAGACTGTACCTGGTGACTAGACACGCTGATGTGGTGCTGGTGGGA
GGAGTGCTGGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTTTCCTGCTGCTGGCTGATGCTAGAGTGTGGATGAAC
AGACTGATCGCTTTCGCTTGTACATGTGGAAGCTCCGATCTGTATCTGAGCGCTTTCAGCCTGCACAGCTACGGAGTG
GCTGGAGCTCTGGTGGCTTTTAAGCTGCCTGGATGTAGCTTTAGCATCTTTAAGACCAGCGAAAGAAGCCAGCCTAGA
CTGATCTTTTGTCACAGCAAGAAGAAGTTTTGGGCTAAGCACATGTGGAATTTTATCCCTTTCTATGGAAAGGCTATC
AGAATGTATGTGGGAGGAGTGGAACACAGACAGCTGTTTACATTTAGCCCTAGAAGGAGACTGGGAGTGAGAGCTACA
AGAAAGGTGGGAATCTATCTGCTGCCTAATAGATGAAAGCTTGGG*

HCV.2

MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAALLFLLLADALIFCHSKKKQLFTFSPRRYLVTRHA
DVYLLPRRGPRLCTCGSSDLYHMWNFISGIFWAKHMWNFAKFVAAWTLKAAAILAGYGAGVYLVAYQATVGVAGALVA
FKIPFYGKAIRMYVGGVEHRVLVGGVLAAFLLLADARVLPGCSFSIFAKFVAAWTLKAAAKTSERSQPRRLGVRATRK
RLIVFPDLGVWMNRLIAFALSAFSLHSYLLFNILGGWVVGIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAGATCTGATGGGATATATCCCTCTGGTGGCTAAGTTTGTGGCTGCTTGGACACTGAAGGCTGCTGCTCTGCTGTTT
CTGCTGCTGGCTGATGCTCTGATCTTCTGTCACAGCAAGAAGAAGCAGCTGTTTACATTTAGCCCAAGAAGATATCTG
GTGACAAGACACGCTGATGTGTATCTGCTGCCTAGACGCGGACCTAGACTGTGTACATGTGGAAGCTCCGATCTGTAT
CACATGTGGAACTTTATCAGCGGAATCTTTTGGGCTAAGCACATGTGGAATTTCATCCTGGCTGGATATGGAGCTGGA
GTGTATCTGGTGGCTTATCAGGCTACAGTGGGAGTGGCTGGAGCTCTGGTGGCTTTCAAGATCCCATTCTATGGAAAG
GCTATCAGAATGTATGTGGGAGGAGTGGAACACAGAGTGCTGGTGGGAGGAGTGCTGGCTGCTTTCCTGCTGCTGGCT
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AGAGCTACAAGGAAGAGACTGATCGTGTTTCCAGATCTGGGAGTGTGGATGAATAGACTGATCGCTTTCGCTCTGAGC
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TGAAAGCTT

HCV.3s1

MGMQVQIQSLFLLLLWVPGSRGYLVAYQATVAKFVAAWTLKAAALLFLLLADALIFCHSKKKYLVTRHADVLGFGAYM
SKCTCGSSDLYHMWNFISGIFWAKHMWNF*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGATACCTCGTCGCCTACCAGGCCACTGTGGCTAAATTCGTGGCAGCCTGGACACTGAAAGCTGCAGCTCTGCTCTTC
CTGCTCCTGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACGTGCTGGGG
TTTGGCGCCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATCTTT
TGGGCCAAGCACATGTGGAATTTCTGAAAGCTT

HCV.3s2
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYILAGYGAGVWM
NRLIAFAIPFYGKAIVAGALVAFKVGIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGAT
CCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTCGCTGCTTGGACACTGAAGGCAGCCGC
TTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGC
GCAGGCGTGTGGATGAATCGGCTGATCGCCTTTGCCATTCCATTCTATGGAAAGCCATTGTGGCTGGCGCCC
TGGTGGCATTCAAGGTCGGGATCTACCTCCTGCCTAACCGCTGAAAGCTT

HCV.3s2(-3)
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYILAGYGAGVWM
NRLIAFA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGAT
CCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTCGCTGCTTGGACACTGAAGGCAGCCGC
TTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGC
GCAGGCGTGTGGATGAATCGGCTGATCGCCTTTGCCTGAGGATCC

HCV.3s3
MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAARLGVRATRKLLFNILGGWVRMYVGGVEHR
RLIVFPDLGVGVAGALVAFKLPGCSFSIFKTSERSQPRQLFTFSPRRYLLPRRGPRL

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGAT
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CAGACTGGGAGTGCGCGCTACACGGAAACTCCTGTTTAACATCCTGGGAGGGTGGGTGCGGATGTACGTCGGA
GGCGTCGAGCACAGAAGGCTCATTGTCTTTCCAGATCTCGGCGTGGGCGTCGCAGGCGCACTCGTGGCCTTCA
AACTGCCAGGGTGCAGCTTCAGCATTTTCAAGACCTCCGAACGCTCCCAACCCAGACAGCTGTTCACTTTCTC
TCCTCGGAGGTATCTGCTGCCCAGACGCGGACCCAGGCTGTGAAAGCTT

HCV.PC3
MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVKAKFVAAWTLKAAALADGGCSGGAYRLIVFPDLGVKFWAKH
MWNFIGVAGALVAFKKQLFTFSPRR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGAT
CCAGAGGACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGC
TGCCGCTCTGGCCGACGGGGGATGCAGCGGCGGAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAA
TTTTGGGCAAAGCACATGTGGAATTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCA
CCTTCTCCCCAAGACGGTGAGGTACC

HCV.PC4

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAKFVAAWTLKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPL
VKYLLPRRGPRLNTLCGFADLMGYRMYVGGVEHR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGAT
CCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGC
CGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCATG
GGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGCCTGAACACTCTCTGTGGATTTGCTG
ATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGATGAGGTACC

HCV.2431(1P)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFAGAAAR
LGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPRRGPRLNTLCGFADLMGYRMYVGGVEH
RKLLFNILGGWVKAAALADGGCSGGAYRLIVFPDLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRRNGYLV
AYQATVAAALLFLLLADALIFCHSKKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFK
AAAAKFVAAWTLKAAA

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGCT
CCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGC
CTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTTGCC
GGCGCTGCCGCAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGC
CCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCT
GCTCCCCAGACGGGGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTATGTC
GGCGGAGTCGAACACAGAAAACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACG
GGGGATGCAGCGGCGGAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACAT
GTGGAATTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAAGACGG
AACGGATACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTTCCTGCTCCTGGCCGATGCACTCA
TCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAG
CAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATCTTTTGGGCCAAGCAC
ATGTGGAATTTTAAGGCCGCAGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGGATCC

FIG.18F

HCV.4312(1P)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPRRGPRLNTLC
GFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFPDLGVKFWAKHMWNFIGVAGALVAFKKQLF
TFSPRRNGYLVAYQATVAAALLFLLLADALIFCHSKKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKH
MWNFKKAAAVLVGGVLAAAFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFANAAAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGCTCCAGAG
GAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGG
ATGCTCTTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGC
CTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGAAAACTGCTCT
TCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCGGAGCTTACAGGCTCATTGT
CTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGAATTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTT
AAAAAGCAGCTCTTCACCTTCTCCCCAAGACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGC
TCTTCCTGCTCCTGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACGTGCT
GGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATC
TTTTGGGCCAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAGTCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGC
TCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGAT
GAATCGGCTGATCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGGATCC

AOSI.K

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVKFLLSLGIHLYMDDVVLGVGLSR
YVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWLSLLVPFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCCTGTGGA
AGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCCTAGCGATTTCTT
TCCTAGCGTGAAGTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGG
TACGTGGCTAGGCTGTTCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGTGA

HBV.1

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVFLLSLGIHLYMDDVVLGVGLSRY
VARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWLSLLVPFVIPIPSSWAFTPARVTGGVFKVGNFTGLYLPSDFFPS
VTLWKAGILYKNVSIPWTHKLVVDFSQFSRSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCCTGTGGA
AGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCCTAGCGATTTCTT
TCCTAGCGTGTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGGTAC
GTGGCTAGGCTGTTCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCCT
TCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGATCCCTATCCCTAGCTCCTGGGCTTTCAC
CCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAAACTTCACCGGCCTGTATCTGCCCAGCGATTTCTTTCCTAGC
GTGACCCTGTGGAAGGCCGGGATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGCTGGTGGTGGACTTTTCCC
AGTTCAGCAGATCCGCTATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGTATGCCTGTATCTGA

HBV.2

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIHLYMDDVVLGVGLSR
YVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIPSSWAFKTPARVTGGVFKVGNFTGLYN
LPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQFSRNSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCCTGTGGA
AGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCCTAGCGATTTCTT
TCCTAGCGTGAACTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGG
TACGTGGCTAGGCTGTTCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGTGAATATCCCTATCCC
TAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAAACTTCACCGGCCTGTATAAC
CTGCCCAGCGATTTCTTTCCTAGCGTGAAGACCCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGA
CCCACAAGGGAGCCGCTCTGGTGGTGGACTTTTCCCAGTTCAGCAGAAATTCCGCTATCTGCTCCGTGGTGAGGAGAGC
TCTGATGCCACTGTATGCCTGTATCTGA

PfCTL.1

MQVQIQSLFLLLLWVPGSRGILSVSSFLFVNAAAQTNFKSLLRNLPSENERGYKAAALLACAGLAYKKAAAAKFVAAWT
LKAAAKAFMKAVCVEVNAAASFLFVEALFNATPYAGEPAPFKAAAKYKLATSVLKAGVSENIFLKNAAAYFILVNLLIK
AGLLGVVSTV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAATCCTGAGCGTGT
CCTCTTTCCTGTTTGTCAACGCCGCTGCACAGACCAATTTCAAGAGCCTCCTGAGGAACCTCCCCTCCGAGAACGAAAG
AGGCTACAAAGCCGCTGCACTGCTCGCCTGCGCTGGACTGGCCTATAAGAAAGCCGCTGCAGCCAAGTTCGTGGCCGCT
TGGACACTGAAGGCCGCTGCAAAAGCCTTTATGAAGGCTGTCTGTGTGGAGGTCAATGCCGCTGCATCTTTCCTGTTTG
TGGAGGCCCTCTTTAACGCTACTCCTTACGCAGGGGAACCAGCCCCCTTCAAGGCCGCTGCAAAATATAAGCTGGCAAC
CAGCGTGCTGAAGGCTGGCGTGTCCGAGAATATTTTTCTGAAAAACGCCGCTGCATACTTCATCCTGGTGAATCTGCTC
ATTAAGGCCGGACTCCTGGGGGTGGTCTCTACAGTGTGA

PfCTL.2

MQVQIQSLFLLLLWVPGSRGFVEALFQEYNAAAKYLVIVFLINALACAGLAYKKFYFILVNLLKAALFFIIFNKNAAAK
FVAAWTLKAAAKFILVNLLIFHNFQDEENIGIYKLPYGRTNLKAAAVLLGGVGLVLNFLIFFDLFLVKAVLAGLLGVV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGATTCGTGGAGGCCC
TGTTTCAGGAATACAACGCCGCTGCAAAGTATCTCGTCATCGTGTTCCTGATCAATGCTCTGGCATGCGCCGGCCTCGC
TTACAAAAAGTTTTACTTCATTCTGGTCAACCTGCTCAAGGCCGCTCTGTTCTTTATCATTTTCAATAAAAACGCCGCA
GCTAAGTTTGTGGCCGCATGGACCCTGAAGGCCGCTGCAAAATTCATCCTCGTGAATCTGCTCATTTTTCACAACTTCC
AAGACGAGGAAAATATCGGAATTTATAAGCTGCCCTACGGGAGGACAAACCTGAAAGCCGCTGCAGTCCTGCTCGGCGG
AGTGGGGCTGGTGCTCAATTTTCTGATCTTCTTTGATCTGTTCCTGGTGAAGGCCGTCCTGGCCGGCCTGCTCGGAGTC
GTGTGA

FIG.18H

PfCTL.3

MQVQIQSLFLLLLWVPGSRGVFLIFFDLFLNAAAPSDGKCNLYKAAAVTCGNGIQVRKLFHIFDGDNEIKAHVLSHNSY
EKNYYGKQENWYSLKKILSVFFLANAAAKFIKSLFHIFKAAALYISFYFIKAKFVAAWTLKAAAKAAAYYIPHQSSLKA
AAGLIMVLSFL

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAGTGTTCCTGATCT
TCTTTGACCTGTTCCTGAACGCCGCTGCACCCAGCGATGGCAAGTGCAATCTCTACAAGGCCGCTGCAGTGACCTGTGG
AAACGGGATTCAGGTCAGGAAACTCTTTCACATCTTCGACGGCGATAACGAGATCAAGGCCCATGTGCTGTCCCACAAT
TCTTATGAAAAAAACTACTATGGAAAGCAAGAGAATTGGTACAGCCTGAAGAAAATTCTGTCCGTGTTCTTTCTCGCCA
ACGCCGCTGCAAAGTTTATCAAGTCTCTGTTCCATATTTTCAAGGCCGCTGCACTCTACATCAGCTTCTATTTTATTAA
AGCCAAATTTGTGGCCGCTTGGACACTGAAGGCCGCTGCAAAAGCCGCTGCATACTATATCCCTCACCAGAGCTCCCTG
AAGGCCGCTGCAGGGCTGATCATGGTGCTCTCTTTCCTGTGA

PfCTL/HTL(N)

MQVQIQSLFLLLLWVPGSRGSSVFNVVNSSIGLIMVLSFLGPGPGLYISFYFILVNLLIFHINGKIIKNSEGPGPGPDS
IQDSLKESRKLSGPGPGVLAGLLGVVSTVLLGGVGLVLGPGPGLPSENERGYYIPHQSSLGPGPGQTNFKSLLRNLGVS
ENIFLKGPGPGFQDEENIGIYGPGPGKYLVIVFLIFFDLFLVGPGPGKFIKSLFHIFDGDNEIGPGPGKSKYKLATSVL
AGLLGPGPGLPYGKTNLGPGPGRHNWVNHAVPLAMKLIGPGPGMRKLAILSVSSFLFVEALFQEYGPGPGVTCGNGIQV
RGPGPGMNYYGKQENWYSLKKGPGPGPSDGKCNLYADSAWENVKNVIGPFMKAVCVEVGPGPGKILSVFFLALFFIIFN
KGPGPGHVLSHNSYEKGPGPGKYKIAGGIAGGLALLACAGLAYKFVVPGAATPYAGEPAPF

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAGTAGTGTGTTCA
ATGTTGTGAACTCATCAATTGGTCTGATCATGGTGCTGAGCTTTCTCG
GGCCAGGGCCAGGATTATATATTTCTTTCTACTTCATCCTTGTCAACCTGTTAATATTCCACATTAACGGCAAAATAAT
AAAGAACAGTGAAGGCCCTGGGCCTGGGCCTGACTCGATCCAGGATTCTCTAAAAGAATCGAGGAAGCTCTCCGGACCA
GGCCCTGGTGTACTCGCCGGGTTGCTGGGAGTAGTTAGCACAGTGCTGTTAGGAGGCGTCGGCCTCGTCTTAGGACCTG
GACCAGGTCTGCCGTCCGAAAACGAAAGAGGATACTACATACCTCACCAGAGCAGCCTCGGCCCAGGCCCCGGACAAAC
CAATTTCAAATCCCTCTTGCGAAATCTAGGAGTGAGCGAGAACATATTTCTTAAAGGACCCGGTCCCGGCTTTCAGGAC
GAGGAGAATATAGGTATTTACGGTCCAGGACCTGGAAAATACCTAGTGATCGTATTCCTAATTTTTTTTGACCTATTTC
TGGTGGGCCCAGGTCCCGGAAAGTTCATTAAATCACTCTTCCACATTTTTGACGGAGATAACGAGATAGGACCCGGTCC
CGGGAAATCAAAGTACAAACTAGCCACTTCAGTGCTGGCCGGCCTTCTAGGGCCGGGCCCAGGGCTCCCCTATGGAAAG
ACAAATCTTGGCCCCGGTCCAGGACGGCACAACTGGGTGAATCATGCGGTTCCATTGGCCATGAAACTAATCGGGCCCG
GTCCAGGCATGCGCAAACTTGCAATTCTAAGCGTAAGTTCATTTCTGTTCGTAGAGGCACTGTTTCAAGAATATGGCCC
AGGACCTGGCGTCACATGTGGGAATGGGATCCAGGTGAGAGGACCGGGACCTGGTATGAACTATTACGGTAAACAGGAA
AATTGGTACTCCCTGAAAAAGGGTCCAGGCCCCGGCCCCTCAGATGGTAAGTGCAACCTGTATGCTGACTCAGCATGGG
AGAACGTAAAAAATGTAATAGGCCCATTCATGAAGGCAGTTTGTGTCGAAGTCGGACCAGGCCCAGGAAAAATACTTTC
TGTCTTCTTCCTAGCTCTCTTCTTCATCATCTTCAACAAGGGACCAGGGCCAGGTCACGTGTTATCCCATAACTCTTAT
GAAAAAGGGCCAGGACCTGGGAAATACAAAATCGCAGGAGGGATCGCCGGCGGGCTAGCGCTCCTTGCCTGCGCAGGCT
TGGCTTACAAATTCGTTGTACCAGGAGCTGCAACACCCTATGCAGGAGAACCTGCCCCATTTTGAAGATCTGC

FIG. 18I

Pf33

MGMQVQIQSLFLLLLWVPGSRGFMKAVCVEVNVTCGNGIQVRKGLIMVLSFLNAALFHIFDGDNEIKAALLACAGLAYK
KSFLFVEALFNAAPSDGKCNLYKAAQTNFKSLLRNLPSENERGYKAAGVSENIFLKNAAAYFILVNLLIKAAAILSVSS
FLFVNTPYAGEPAPFKAAAKYKLATSVLKAAVFLIFFDLFLNYYIPHQSSLKAAGLLGNVSTVGAVLLGGVGLVLNLAC
AGLAYKKAKFIKSLFHIFKAAFYFILVNLLKAFLIFFDLFLVKALFFIIFNKNYYGKQENWYSLKFVEALFQEYNAAAK
FVAAWTLKAAAKILSVFFLANAVLAGLLGNVNFQDEENIGIYKAAALYISFYFIKAFILVNLLIFHNAALPYGRTNLKA
AHVLSHNSYEKNAAAKYLVIVFLI

GCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGATTTA
TGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCGGTAACGGAATTCAGGTGAGAAAGGGACTCATCATGGTACTCAG
CTTTCTGAACGCAGCCCTGTTCCACATCTTTGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGGACTA
GCCTATAAAAAGAGTTTCCTTTTCGTTGAAGCACTATTTAACGCAGCACCCAGTGACGGTAAATGCAACCTATATAAAG
CAGCTCAGACTAATTTCAAAAGCCTGTTAAGAAATCTGCCCTCAGAGAATGAAAGGGGTTACAAAGCCGCCGGCGTGTC
CGAGAATATTTTCCTGAAGAACGCCGCTGCTTATTTTATACTCGTGAATCTACTCATAAAGGCAGCCGCAATCCTTTCA
GTGTCCAGCTTTCTGTTTGTTAACACACCATATGCGGGCGAGCCGGCTCCTTTCAAGGCTGCAGCAAAATACAAGCTTG
CCACATCAGTATTGAAAGCAGCTGTGTTTTTGATATTCTTTGATCTTTTTTTAAACTACTACATACCTCATCAGTCTAG
TCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCCGTCTTACTTGGAGGAGTTGGCCTCGTGTTGAAC
CTCGCGTGCGCAGGTCTGGCCTACAAAAAAGCGAAATTCATCAAGTCTCTGTTCCACATTTTTAAAGCCGCATTCTATT
TCATACTAGTGAACCTTCTCAAAGCTTTCCTGATCTTCTTCGATCTATTCCTCGTAAAAGCGCTATTCTTCATTATCTT
TAACAAAAATTATTACGGCAAGCAAGAAAATTGGTACTCACTCAAGTTTGTAGAAGCTCTGTTCCAGGAATACAACGCC
GCTGCTAAATTCGTTGCAGCTTGGACCCTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTTCTCGCTAATGCCGTAT
TAGCAGGACTTCTAGGCAACGTGAACTTTCAAGACGAAGAGAATATAGGCATCTACAAAGCCGCAGCACTGTACATTTC
ATTCTACTTCATCAAGGCCTTCATACTGGTCAACCTTCTGATATTTCATAATGCAGCACTGCCATATGGGAGAACCAAC
TTGAAAGCGGCCCACGTGTTGAGCCACAACTCCTACGAGAAGAACGCCGCCGCGAAATATCTCGTCATTGTCTTCCTGA
TTTGA

TB.1

MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNLMIGTAAAVVKALVLLMLPVGAGLMTAVYLVGAAAMA
LLRLPVKRMFAANLGVNSLYFGGICVGRLPLVLPAVNAAAAKFVAAWTLKAAAKAAARLMIGTAAAGFVVALIPLVNAM
TYAAPLFVGAAAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAGGATGAGCAGAGTGACCA
CATTCACTGTCAAGGCCCTGGTGCTCCTGATGCTCCCCGTCGTGAACCTGATGATCGGCACCGCTGCAGCCGTCGTGAA
AGCTCTCGTCCTGCTCATGCTCCCTGTGGGAGCAGGGCTGATGACAGCCGTGTACCTGGTCGGCGCTGCAGCCATGGCC
CTCCTGCGGCTGCCAGTGAAGCGCATGTTTGCTGCAAATCTGGGAGTCAACTCCCTCTATTTCGGGGGCATTTGCGTGG
GAAGGCTGCCCCTCGTGCTGCCTGCTGTGAATGCAGCCGCTGCCAAATTTGTCGCCGCTTGGACTCTGAAGGCAGCCGC
TAAGGCCGCTGCAAGACTGATGATCGGGACCGCCGCTGCCGGCTTCGTGGTCGCCCTGATTCCCCTGGTGAACGCCATG
ACATACGCAGCTCCTCTGTTTGTGGGAGCCGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA

FIG.18J

BCL A2 #90

MQVQIQSLFLLLLWVPGSRGIMIGHLVGVNRLLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYLSGANLNVG
AAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTRVNAAAATVGIMIGVNAKLCPVQL
WV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAATTATGATCGGCC
ATCTGGTGGGCGTCAACAGACTGCTGCAGGAAACCGAGCTGGTGAATGCCAAGGTGGCCGAAATTGTGCACTT
TCTCAACGCAAAGGTGTTTGGTTCCCTGGCTTTTGTCAATGCCTATCTGAGCGGCGCTAACCTCAACGTCGGA
GCCGCCTACCTCCAGCTGGTCTTCGGCATCGAGGTCAACGCTGCTGCAAAATTCGTGGCAGCTTGGACCCTCA
AGGCTGCAGCAAAGGCTGCCGCCGTCGTGCTCGGAGTGGTGTTCGGGATCAACTCTATGCCACCTCCCGGGAC
TAGGGTCAATGCTGCCGCCGCAACAGTGGGAATCATGATTGGGGTGAATGCCAAACTGTGCCCAGTGCAACTG
TGGGTGTGA

BCL A2 #88

MQVQIQSLFLLLLWVPGSRGVVLGVVFGINAAAAKFVAAWTLKAAAKVAEIVHFLNAYLSGANLNVGAAYLQL
VFGIEVNIMIGHLVGVNRLLQETELVNAKVFGSLAFVNAKLCPVQLWVNAAAATVGIMIGVNSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAGTCGTGCTGGGAG
TCGTCTTCGGCATTAATGCCGCCGCTGCAAAGTTCGTGGCTGCCTGGACCCTGAAGGCCGCAGCTAAAGTGGC
AGAGATCGTGCACTTTCTGAACGCCTACCTGAGCGGAGCAAATCTGAACGTCGGCGCTGCCTATCTGCAGCTC
GTGTTTGGAATTGAAGTGAACATCATGATTGGACATCTGGTGGGCGTGAACAGGCTGCTCCAGGAAACTGAGC
TGGTCAACGCTAAAGTGTTCGGGTCTCTCGCCTTTGTGAACGCTAAGCTCTGCCCCGTCCAACTCTGGGTCAA
TGCCGCAGCCGCTACAGTGGGGATCATGATCGGCGTGAACTCCATGCCTCCACCAGGGACCAGAGTGTGA

BCL A2 #63

MQVQIQSLFLLLLWVPGSRGKLCPVQLWVNAAAATVGIMIGVNIMIGHLVGVNRLLQETELVNAKVAEIVHFL
NAKVFGSLAFVNAYLSGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTR
V

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAAAGCTCTGCCCCG
TGCAACTGTGGGTCAACGCCGCCGCCGCAACCGTCGGCATTATGATCGGGGTGAACATCATGATCGGACACCT
GGTCGGCGTGAACAGGCTGCTGCAGGAGACAGAACTGGTCAATGCCAAGGTGGCTGAAATTGTCCATTTCCTG
AATGCCAAAGTGTTCGGCTCTCTCGCTTTCGTGAACGCTTATCTGAGCGGAGCTAACCTCAACGTGGGGGCCG
CATACCTCCAGCTCGTCTTTGGGATTGAGGTGAATGCCGCAGCTAAATTTGTCGCTGCCTGGACCCTGAAGGC
AGCAGCCAAGGCTGCCGCAGTGGTGCTGGGAGTGGTGTTTGGAATCAATTCCATGCCTCCACCAGGCACTAGA
GTGTGAGGATCC

FIG.18K

Prostate 1
LTFFWLDRSVKAAAVLVHPQWVLTVKAAALLQERGVAYIKAALLLSIALSVNPLVCNGVLQGVKAAIMYSAHD
TTVKAAAFLTPKKLQCVNAMMNDQLMFLNAGLPSIPVHPVKAAALGTTCYVGAAILLWQPIPVNFLRPRSLQC
VKAFLTLSVTWIGVNALLYSLVHNLGAATLMSAMTNL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATTGACATTTTTTT
GGCTGGATAGATCGGTTAAGGCTGCAGCCGTGCTTGTTCATCCCCAGTGGGTCTTGACCGTAAAGGCTGCCGC
GCTGCTACAAGAAAGAGGGGTCGCATACATCAAAGCTGCTCTCCTCTTGAGTATTGCGCTAAGTGTAAACCCG
CTAGTTTGTAATGGGGTGTTACAAGGTGTGAAAGCGGCGATTATGTACAGTGCCCACGACACTACCGTAAAAG
CAGCCGCTTTCCTGACCCCAAAAAAACTCCAATGCGTGAACGCAATGATGAATGATCAGCTGATGTTTTTAAA
CGCTGGCTTACCTTCTATACCGGTTCATCCAGTCAAGGCCGCGGCATTGGGTACGACGTGTTATGTTGGAGCA
GCGATACTTCTTTGGCAGCCCATACCAGTAAATTTTTTAAGACCTAGATCCTTACAATGCGTCAAAGCATTCC
TTACACTCTCAGTAACTTGGATCGGAGTCAATGCTCTGCTATATAGCCTCGTACACAACTTGGGCGCGGCCAC
ACTTATGAGTGCAATGACGAATTTAGCTAAGTTCGTGGCGGCCTGGACTCTAAAGGCCGCAGCA

HIV-1043
MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGPGPGWEFVNTPPLVKLWYQGPGPGYRKILRQRKID
RLIDGPGPGQHLLQLTVWGIKQLQGPGPGGEIYKRWIILGLNKIVRMYGPGPGQGQMVHQAISPRTLNGPGPG
IKQFINMWQEVGKAMYGPGPGWAGIKQEFGIPYNPQGPGPGKTAVQMAVFIHNFKRGPGPGSPAIFQSSMTKI
LEPGPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPPGPGPGAETFYVDGAANRETKGPGPGGAVVI
QDNSDIKVVPGPGPGFRKYTAFTIPSINNE

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCGGACCTGGGCAGAAAC
AGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAGGTTGGGAGTTTGTGAACACACC
ACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGATACCGTAAAATCCTGAGGCAAAGAAAGATAGAT
CGCCTCATTGATGGCCCGGGCCCAGGCCAGCACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAGCTGCAGG
GGCCGGGCCCCGGGGGGGAAATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGG
CCCTGGACCCGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGCCCAGGA
ATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTGGATGGGCAGGGA
TAAAACAGGAGTTTGGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGTAAAACGGCAGTGCAGATGGCCGT
GTTCATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGCCCAGCTATATTTCAAAGTTCGATGACCAAAATC
TTGGAGCCCGGCCCAGGGCCGGGCGAAGTGAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGC
CCGGACCAGGGCATTCCAATTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGC
GGAAACTTTCTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCATT
CAGGACAACTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCCGGGTTCAGAAAGTATACCGCCTTCACTATTC
CGTCCATCAACAATGAGTGA

FIG. 18L

HIV-1043 PADRE

MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGPGPGWEFVNTPPLVKLWYQGPGPGYRKILRQRKID
RLIDGPGPGQHLLQLTVWGIKQLQGPGPGGEIYKRWIILGLNKIVRMYGPGPGQGQMVHQAISPRTLNGPGPG
IKQFINMWQEVGKAMYGPGPGWAGIKQEFGIPYNPQGPGPGKTAVQMAVFIHNFKRGPGPGSPAIFQSSMTKI
LEPGPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPPGPGPGAETFYVDGAANRETKGPGPGGAVVI
QDNSDIKVVPGPGPGFRKYTAFTIPSINNEGPGPGAKFVAAWTLKAAA

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCGGACCTGGGCAGAAAC
AGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAGGTTGGGAGTTTGTGAACACACC
ACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGATACCGTAAAATCCTGAGGCAAAGAAAGATAGAT
CGCCTCATTGATGGCCCGGGCCCAGGCCAGCACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAGCTGCAGG
GGCCGGGCCCCGGGGGGGAAATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGG
CCCTGGACCCGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGCCCAGGA
ATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTGGATGGGCAGGGA
TAAAACAGGAGTTTGGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGTAAAACGGCAGTGCAGATGGCCGT
GTTCATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGCCCAGCTATATTTCAAAGTTCGATGACCAAAATC
TTGGAGCCCGGCCCAGGGCCGGGCGAAGTGAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGC
CCGGACCAGGGCATTCCAATTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGC
GGAAACTTTCTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCATT
CAGGACAACTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCCGGGTTCAGAAAGTATACCGCCTTCACTATTC
CGTCCATCAACAATGAGGGCCCCGGCCCAGGTGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTG
A

HIV 75mer

EKVYLAWVPAHKGIGGPGPGQGQMVHQAISPRTLNGPGPGSPAIFQSSMTKILEPGPGPGFRKYTAFTIPSIN
NE

GAGAAGGTGTACCTGGCCTGGGTGCCTGCCCACAAGGGAATCGGAGGACCTGGCCCTGGACAGGGACAGATGG
TGCACCAGGCCATCAGCCCTAGGACCCTGAACGGACCTGGACCTGGAAGCCCTGCCATCTTCCAGAGCAGCAT
GACCAAGATCCTGGAGCCCGGACCTGGACCTGGATTCAGGAAGTACACCGCCTTCACCATCCCCAGCATCAAC
AACGAGTGA

FIG.18M

PfHTL

MQVQIQSLFLLLLWVPGSRGRHNWVNHAVPLAMKLIGPGPGKCNLYADSAWENVKNGPGPGKSKYKLATSVL
AGLLGPGPGQTNFKSLLRNLGVSEGPGPGSSVFNVVNSSIGLIMGPGPGVKNVIGPFMKAVCVEGPGPGMNY
YGKQENWYSLKKGPGPGGLAYKFVVPGAATPYGPGPGPDSIQDSLKESRKLNGPGPGLLIFHINGKIIKNSE
GPGPGAGLLGNVSTVLLGGVGPGPGKYKIAGGIAGGLALLGPGPGMRKLAILSVSSFLFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAGGCAC
AACTGGGTGAATCATGCTGTGCCCCTGGCTATGAAGCTGATCGGCCCTGGACCAGGGAAATGCAACCTCTAC
GCAGACAGCGCCTGGGAGAACGTCAAGAATGGCCCCGGACCTGGGAAATCCAAGTATAAGCTCGCTACCTCT
GTGCTGGCAGGCCTGCTCGGACCAGGCCCCGGACAGACAAATTTCAAAAGCCTGCTCAGAAACCTGGGAGTG
TCCGAGGGGCCTGGCCCAGGATCTAGCGTCTTTAATGTGGTCAACTCCTCTATTGGGCTCATCATGGGACCC
GGACCTGGGGTGAAAAATGTCATTGGCCCATTCATGAAGGCCGTGTGTGTCGAAGGACCCGGGCCTGGCATG
AACTACTATGGAAAGCAAGAAAATTGGTACAGCCTGAAGAAAGGCCCTGGGCCAGGCGGACTGGCTTACAAG
TTTGTGGTCCCAGGGGCAGCCACTCCCTATGGGCCTGGGCCAGGCCCCGATTCCATCCAGGACTCTCTCAAA
GAGAGCCGGAAACTGAACGGACCCGGGCCTGGACTGCTCATTTTCCACATCAATGGCAAAATTATCAAGAAC
AGCGAGGGACCTGGGCCAGGCGCCGGACTGCTGGGGAACGTGTCCACCGTCCTGCTCGGCGGAGTGGGGCCC
GGCCCTGGGAAGTACAAGATCGCTGGAGGGATCGCAGGCGGACTGGCCCTCCTGGGCCCAGGACCAGGGATG
CGCAAACTGGCTATTCTCTCTGTCTCCAGCTTTCTGTTTGTGTGA

FIG. 18N

Protein	Sequence	Restriction
HIV gag 386	VLAEAMSQV	HLA-A2
HIV gag 271	MTNNPPIPV	HLA-A2
HIV pol 774	MASDFNLPPV	HLA-A2
HIV pol 448	KLVGKLNWA	HLA-A2
HIV pol 163	LVGPTPVNI	HLA-A2
HIV pol 498	ILKEPVHGV	HLA-A2
HIV pol 879	KAACWWAGI	HLA-A2
HIV pol 132	KMIGGIGGFI	HLA-A2
HIV pol 772	RAMASDFNL	HLA-A2
HIV pol 183	TLNFPISPI	HLA-A2
HIV env 134	KLTPLCVTL	HLA-A2
HIV env 651	LLQLTVWGI	HLA-A2
HIV env 163	SLLNATDIAV	HLA-A2
HIV nef 221	LTFGWCFKL	HLA-A2
HIV vpr 59	AIIRILQQL	HLA-A2
HIV vpr 62	RILQQLLFI	HLA-A2
HIV pol 929	QMAVFIHNFK	HLA-A3
HIV pol 722	KVYLAWVPAHK	HLA-A3
HIV pol 971	KIQNFRVYYR	HLA-A3
HIV pol 347	AIFQSSMTK	HLA-A3
HIV pol 98	VTIKIGGQLK	HLA-A3
HIV env 61	TTLFCASDAK	HLA-A3
HIV env 47	VTVYYGVPVWK	HLA-A3
HIV nef 100	QVPLRPMTYK	HLA-A3
HIV vif 7	VMIVWQVDR	HLA-A3
HIV gag 162	QMVHQAISPR	HLA-A3
HIV gag 545	YPLASLRSLF	HLA-B7
HIV gag 237	HPVHAGPIA	HLA-B7
HIV pol 186	FPISPIETV	HLA-B7
HIV pol 893	IPYNPQSQGVV	HLA-B7
HIV env 259	IPIHYCAPA	HLA-B7
HIV env 250	CPKVSFEPI	HLA-B7
HIV nef 94	FPVRPQVPL	HLA-B7
HIV rev 75	VPLQLPPL	HLA-B7
HIV pol 684	EVNIVTDSQY	HLA-A1
HIV gag 317	FRDYVDRFY	HLA-A1
HIV pol 368	VIYQYMDDLY	HLA-A1
HIV pol 295	VTVLDVGDAY	HLA-A1
HIV pol 533	IYQEPFKNL	HLA-A24
HIV pol 244	PYNTPVFAI	HLA-A24
HIV pol 530	TYQIYQEPF	HLA-A24
HIV pol 597	YWQATWIPEW	HLA-A24
HIV env 681	IWGCSGKLI	HLA-A24
HIV env 671	RYLKDQQLL	HLA-A24

FIG.19A

Protein	Sequence	Restriction
HIV env 55	VWKEATTTLF	HLA-A24
HIV vpr 46	IYETYGDTW	HLA-A24
HIV vpr 14	PYNEWTLEL	HLA-A24
HIV gag 298	KRWIILGLNKIVRMY	HLA-DR
HIV pol 596	WEFVNTPPLVKLWYQ	HLA-DR
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR
HIV env 729	QHLLQLTVWGIKQLQ	HLA-DR
HIV gag 171	QGQMVHQAISPRTLN	HLA-DR
HIV pol 335	SPAIFQSSMTKILEP	HLA-DR
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR
HIV pol 758	HSNWRAMASDFNLPP	HLA-DR
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR
HIV vpu 31	YRKILRQRKIDRLID	HLA-DR3
HIV pol 874	WAGIKQEFGIPYNPQ	HLA-DR3
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3
HIV pol 619	AETFYVDGAANRETK	HLA-DR3
HIV pol 989	GAVVIQDNSDIKVVP	HLA-DR3
HCV NS4 1812	LLFNILGGWV	HLA-A2
HCV NS1/E2 728	FLLLADARV	HLA-A2
HCV NS4 1590	YLVAYQATV	HLA-A2
HCV NS5 2611	RLIVFPDLGV	HLA-A2
HCV CORE 132	DLMGYIPLV	HLA-A2
HCV NS4 1920	WMNRLIAFA	HLA-A2
HCV NS4 1666	VLVGGVLAA	HLA-A2
HCV NS4 1769	HMWNFISGI	HLA-A2
HCV NS4 1851	ILAGYGAGV	HLA-A2
HCV CORE 35	YLLPRRGPRL	HLA-A2
HCV NS1/E2 726	LLFLLLADA	HLA-A2
HCV LORF 1131	YLVTRHADV	HLA-A2
HCV CORE 51	KTSERSQPR	HLA-A3
HCV CORE 43	RLGVRATRK	HLA-A3
HCV ENV1 290	QLFTFSPRR	HLA-A3
HCV NS1/E2 632	RMYVGGVEHR	HLA-A3
HCV NS3 1396	LIFCHSKKK	HLA-A3
HCV NS4 1863	GVAGALVAFK	HLA-A3
HCV NS4 1864	VAGALVAFK	HLA-A3
HCV NS3 1262	LGFGAYMSK	HLA-A3
HCV Core 169	LPGCSFSIF	HLA-B7
HCV NS5 2922	LSAFSLHSY	HLA-A1
HCV NS3 1128	CTCGSSDLY	HLA-A1
HCV NS5 2180	LTDPSHITA	HLA-A1

Protein	Sequence	Restriction
HCV Core 126	LTCGFADLMGY	HLA-A1
HCV NS3 1305	LADGGCSGGAY	HLA-A1
HCV NS4 1765	FWAKHMWNF	HLA-A24
HCV NS5 2875	RMILMTHFF	HLA-A24
HCV NS5 2639	VMGSSYGF	HLA-A24
HCV NS4 1765	FWAKHMWNFI	HLA-A24
P. falciparum SSP2-230	FMKAVCVEV	HLA-A2
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2
P. falciparum CSP-7	ILSVSSFLFV	HLA-A2
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3
P. falciparum LSA1-105	GVSENIFLK	HLA-A3
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7
P. falciparum LSA1-1663	LPSENERGY	HLA-A1
P. falciparum EXP1-73	KYKLATSVL	HLA-A24
P. falciparum CSP-12	SFLFVEALF	HLA-A24
P. falciparum LSA1-10	YFILVNLLI	HLA-A24
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2
P. falciparum SSP2-523	LACAGLAYK	HLA-A3
P. falciparum EXP1-10	ALFFIIFNK	HLA-A3
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3
P. falciparum SSP2-126	LPYGRTNL	HLA-B7
P. falciparum CSP-15	FVEALFQEY	HLA-A1
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1
P. falciparum LSA1-9	FYFILVNLL	HLA-A24
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24
P. falciparum CSP-394	GLIMVLSFL	HLA-A2
P. falciparum EXP1-2	KILSVFFLA	HLA-A2
P. falciparum CSP-344	VTCGNGIQVR	HLA-A3
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24
P. falciparum LSA1-5	LYISFYFI	HLA-A24
P. falciparum CSP-2	MRKLAILSVSSFLFV	HLA-DR
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3

Protein	Sequence	Restriction
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR
P. falciparum SSP2-527	GLAYKFVVPGAATPY	HLA-DR
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR
P. falciparum LSA1-16	LLIFHINGKIIKNSE	HLA-DR
P. falciparum LSA1-94	QTNFKSLLRNLGVSE	HLA-DR
HBV core 18	FLPSDFFPSV	HLA-A2
HBV env 183	FLLTRILTI	HLA-A2
HBV env 335	WLSLLVPFV	HLA-A2
HBV pol 455	GLSRYVARL	HLA-A2
HBV pol 538	YMDDVVLGV	HLA-A2/A1
HBV pol 773	ILRGTSFVYV	HLA-A2
HBV pol 562	FLLSLGIHL	HLA-A2
HBV pol 642	ALMPLYACI	HLA-A2
HBV env 338	GLSPTVWLSV	HLA-A2
HBV core 141	STLPETTVVRR	HLA-A3
HBV pol 149	HTLWKAGILYK	HLA-A3/A1
HBV pol 150	TLWKAGILYK	HLA-A3
HBV pol 388	LVVDFSQFSR	HLA-A3
HBV pol 47	NVSIPWTHK	HLA-A3
HBV pol 531	SAICSVVRR	HLA-A3
HBV pol 629	KVGNFTGLY	HLA-A3/A1
HBV pol 665	QAFTFSPTYK	HLA-A3
HBV core 19	LPSDFFPSV	HLA-B7
HBV env 313	IPIPSSWAF	HLA-B7
HBV pol 354	TPARVTGGVF	HLA-B7
TB	RMSRVTTFTV	HLA-A2
TB	ALVLLMLPVV	HLA-A2
TB	LMIGTAAAVV	HLA-A2
TB	ALVLLMLPV	HLA-A2
TB	GLMTAVYLV	HLA-A2
TB	MALLRLPV	HLA-A2
TB	RMFAANLGV	HLA-A2
TB	SLYFGGICV	HLA-A2
TB	RLPLVLPAV	HLA-A2
TB	RLMIGTAAA	HLA-A2
TB	FVVALIPLV	HLA-A2
TB	MTYAAPLFV	HLA-A2
TB	AMALLRLPLV	HLA-A2
p53 139	KLCPVQLWV	HLA-A2
CEA 687	ATVGIMIGV	HLA-A2
CEA 691	IMIGHLVGV	HLA-A2
Her2/neu 689	RLLQETELV	HLA-A2
MAGE3 112	KVAEIVHFL	HLA-A2

Protein	Sequence	Restriction
Her2/neu 665	VVLGVVFGI	HLA-A2
p53 149	SMPPPGTRV	HLA-A2
PAP.21.T2	LTFFWLDRSV	HLA-A2
PAP.112	TLMSAMTNL	HLA-A2
PAP.284	IMYSAHDTTV	HLA-A2
PSM.288.V10	GLPSIPVHPV	HLA-A2
PSM.441	LLQERGVAYI	HLA-A2
PSM.469L2	LLYSLVHNL	HLA-A2
PSM.663	MMNDQLMFL	HLA-A2
PSA.3.V11	FLTLSVTWIGV	HLA-A2
PSA.143.V8	ALGTTCYV	HLA-A2
PSA.161	FLTPKKLQCV	HLA-A2
HuK2.4.L2	LLLSIALSV	HLA-A2
HuK2.53.V11	VLVHPQWVLTV	HLA-A2
HuK2.165	FLRPRSLQCV	HLA-A2
HuK2.216.V11	PLVCNGVLQGV	HLA-A2

FIG.19E

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN[1]
924.07	core 18	FLPSDFFPSV	45	A2	3.5	5
777.03	env 183	FLLTRILTI	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
1168.02	pol 455	GLSRYVARL	55	A2	55.9	3
1090.77	pol 538	YMDDVVLGV	90	A2/A1	6.4	5
927.11	pol 562	FLLSLGIHL	95	A2	7.8	3
927.15	pol 642	ALMPLYACI	95	A2	12.9	4
1083.01	core 141	STLPETTVVRR	95	A3/A11	735/4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4/15.6	5
1069.15	pol 150	TLWKAGILYK	100	A3/A11	2.1/33	2
1069.20	pol 388	LVVDFSQFSR	100	A3/A11	6875/17	3
1069.16	pol 47	NVSIPWTHK	100	A3/A11	174/117	3
1090.11	pol 531	SAICSVVRR	95	A3/A11	2189/29	3
1142.05	pol 629	KVGNFTGLY	95	A3/A1	58/365	2
1090.10	pol 665	QAFTFSPTYK	95	A3/A11	249/8	3
988.05	core 19	LPSDFFPSV	45	B7	3026.8	4
1145.04	env 313	IPIPSSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPHLL	100	B7	56.6	4
1039.06	env 359	WMMWYWGPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTFGRETVLEY	75	A1	80.0	3
1090.07	pol 415	LSLDVSAAFY	95	A1	6.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.07	core 117	EYLVSFGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3

[1] XRN = Cross binding, number of HLA types in the supertype panel of 5 for which significant binding as detected

FIG.20A

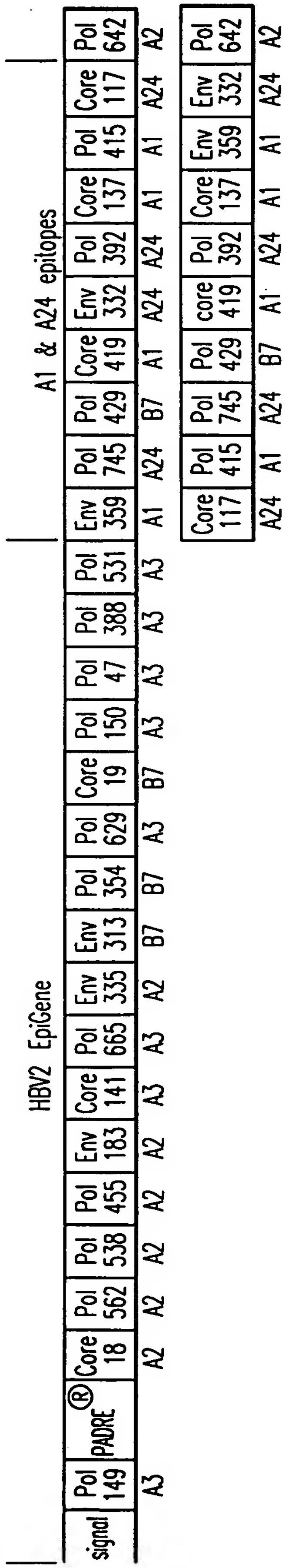

HBV2 EpiGene
A1 & A24 epitopes
signal
Pol 149 A3
PADRE®
Core 18 A2
Pol 562 A2
Pol 538 A2
Pol 455 A2
Env 183 A2
Core 141 A3
Pol 665 A3
Env 335 A2
Env 313 B7
Pol 354 B7
Pol 629 A3
Core 19 B7
Pol 150 A3
Pol 47 A3
Pol 388 A3
Pol 531 A3
Env 359 A1
Pol 745 A24
Pol 429 B7
Core 419 A1
Env 332 A24
Pol 392 A24
Core 137 A1
Pol 415 A1
Core 117 A24
Pol 642 A2
Core 117 A24
Pol 415 A1
Pol 745 A24
Pol 429 B7
core 419 A1
Pol 392 A24
Core 137 A1
Env 359 A1
Env 332 A24
Pol 642 A2

FIG.20B

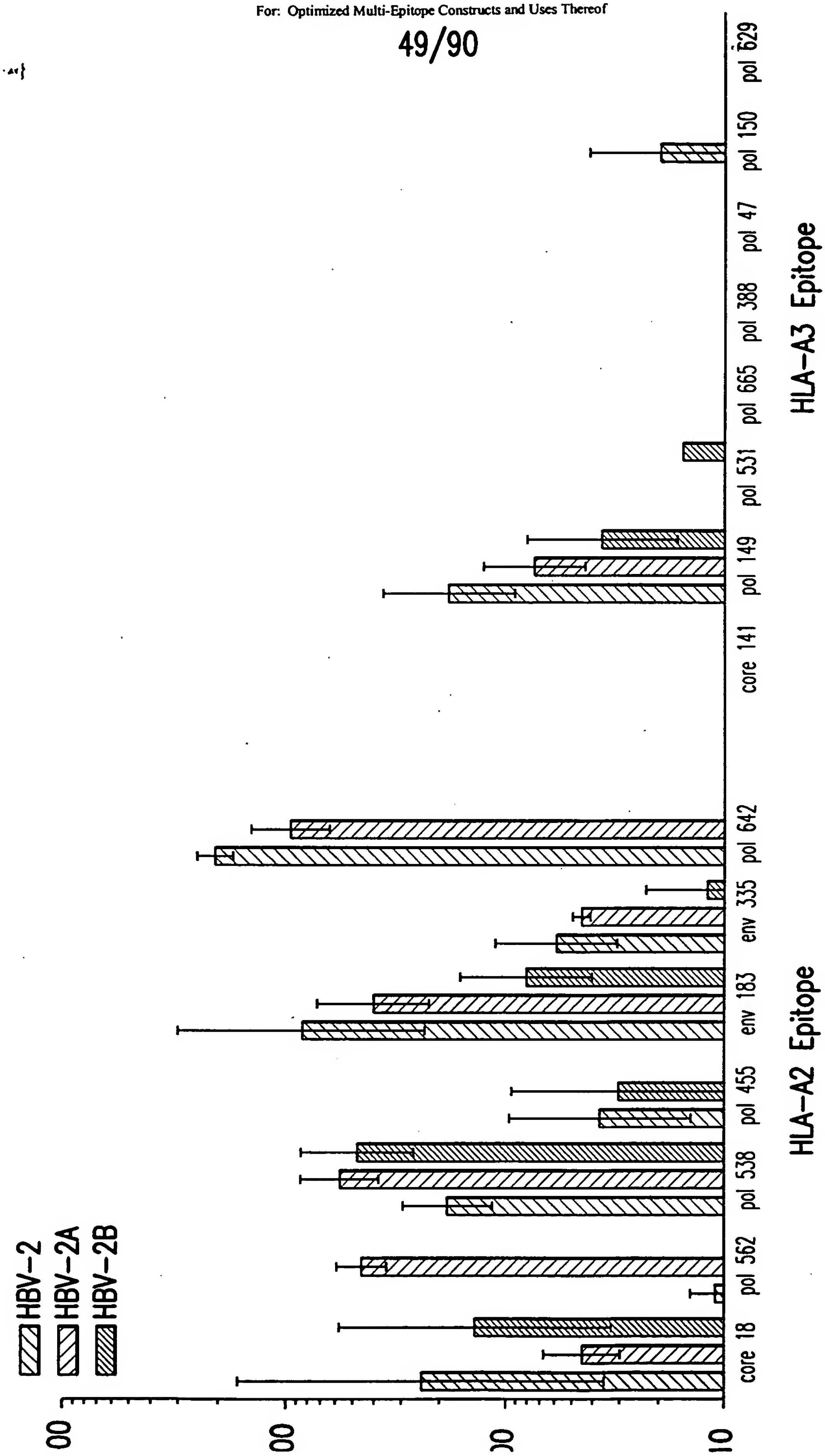

HBV-2
HBV-2A
HBV-2B
10
core 18
pol 562
pol 538
pol 455
env 183
env 335
pol 642
core 141
pol 149
pol 531
pol 665
pol 388
pol 47
pol 150
pol 629
HLA-A2 Epitope
HLA-A3 Epitope

FIG.20C

HBV-2

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIHLYMDDVVLGVGLS
RYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIPSSWAFKTPARVTGGVFKVGNFTGL
YNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQFSRNSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCCTGTGG
AAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCCTAGCGATTTC
TTTCCTAGCGTGAACTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCC
AGGTACGTGGCTAGGCTGTTCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGG
CAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGTGAATATCCCT
ATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAAACTTCACCGGCCTG
TATAACCTGCCCAGCGATTTCTTTCCTAGCGTGAAGACCCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATC
CCTTGGACCCACAAGGGAGCCGCTCTGGTGGTGGACTTTTCCCAGTTCAGCAGAAATTCCGCTATCTGCTCCGTGGTG
AGGAGAGCTCTGATGCCACTGTATGCCTGTATCTGA

FIG.20D

HBV-2A

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIHLYMDDVVLGVGLS
RYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIPSSWAFKTPARVTGGVFKVGNFTGL
YNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQFSRNSAICSVVRRKAWMMWYWGPSLYKKYTSFPWLLN
AHPAAMPHLLKAAADLLDTASALYNAAARFSWLSLLVPFNAASWPKFAVPNLKLTFGRETVLEYKALSLDVSAAFYGA
AEYLVSFGVWGAALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCCTGTGG
AAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCCTAGCGATTTC
TTTCCTAGCGTGAACTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCC
AGGTACGTGGCTAGGCTGTTCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGG
CAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGTGAATATCCCT
ATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAAACTTCACCGGCCTG
TATAACCTGCCCAGCGATTTCTTTCCTAGCGTGAAGACCCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATC
CCTTGGACCCACAAGGGAGCCGCTCTGGTGGTGGACTTTTCCCAGTTCAGCAGAAATAGCGCCATCTGTTCGGTCGTG
AGAAGGAAAGCCTGGATGATGTGGTACTGGGGTCCTAGTCTGTATAAGAAGTACACCTCATTCCCATGGCTCTTGAAT
GCCCATCCCGCTGCAATGCCACACCTGCTTAAAGCTGCGGCGGATCTGCTGGACACAGCCTCAGCTTTATATAATGCT
GCAGCAAGATTCTCCTGGTTGTCTCTCTTAGTGCCCTTCAACGCAGCTTCCTGGCCAAAATTTGCCGTTCCGAACCTG
AAGCTCACTTTTGGAAGAGAGACAGTACTTGAATACAAAGCACTAAGCCTTGACGTGTCAGCAGCCTTCTACGGAGCA
GCAGAATATCTAGTATCTTTTGGGGTCTGGGGCGCAGCCCTCATGCCTCTATACGCCTGCATTTGA

FIG.20E

HBV-2B

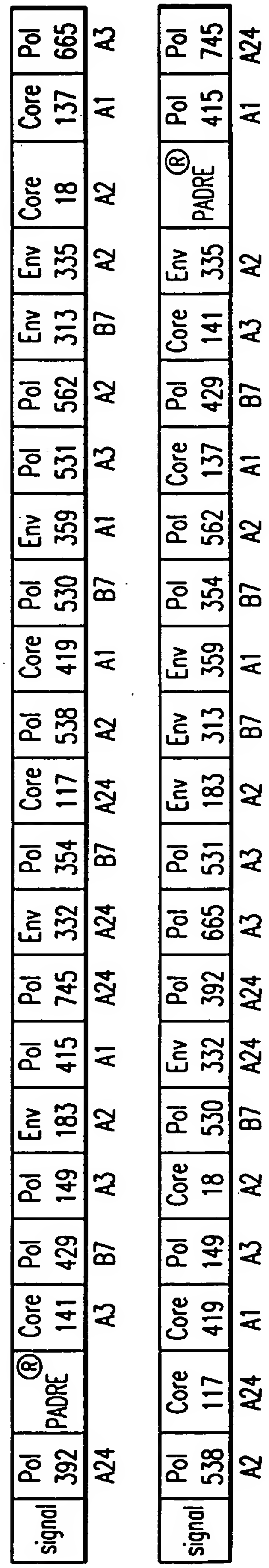
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIHLYMDDVVL
GVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIPSSWAFKTPARVTGG
VFKVGNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQFSRNSAICSVVRRKEYLVSFGV
WGLSLDVSAAFYNAAAKYTSFPWLLNAHPAAMPHLLKAAADLLDTASALYNSWPKFAVPNLKLTFGRETVLEY
KAAWMMWYWGPSLYKAAARFSWLSLLVPFGAAALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCC
TGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCC
TAGCGATTTCTTTCCTAGCGTGAACTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTG
GGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAG
AGACCACCGTGGTGAGGAGGCAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCT
GCTGGTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGA
GTGTTTAAGGTGGGAAACTTCACCGGCCTGTATAACCTGCCCAGCGATTTCTTTCCTAGCGTGAAGACCCTGT
GGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGGTGGTGGACTT
TTCCCAGTTCAGCAGAAATTCAGCAATTTGTTCGGTGGTGAGAAGAAAGGAATATCTTGTTTCATTTGGCGTC
TGGGGGCTGTCACTGGATGTAAGTGCGGCATTTTACAATGCCGCCGCAAAATATACAAGCTTCCCATGGCTCC
TAAACGCACACCCAGCTGCAATGCCGCATCTACTGAAAGCAGCCGCTGACCTCTTAGACACTGCCTCCGCTCT
GTACAACTCTTGGCCCAAGTTTGCCGTGCCTAATCTCAAGTTGACCTTCGGTAGAGAGACAGTCTTAGAATAC
AAAGCGGCCTGGATGATGTGGTACTGGGGACCCTCTCTGTATAAAGCCGCTGCAAGGTTCTCCTGGCTTAGCC
TTCTCGTACCATTCGGAGCAGCTGCCCTAATGCCTTTGTACGCATGCATCTGA

FIG.20F

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN
924.07	core 18	FLPSDFFPSV	45	A2	3.5	5
777.03	env 183	FLLTRILTI	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
927.11	pol 562	FLLSLGIHL	95	A2	7.8	3
1090.77	pol 538	YMDDVVLGV	90	A2/A1	6.4	5
1083.01	core 141	STLPETTVVRR	95	A3/A11	735/4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4/15.6	5
1090.11	pol 531	SAICSVVRR	95	A3/A11	2189/29	3
1090.10	pol 665	QAFTFSPTYK	95	A3/A11	249/8	3
1145.04	env 313	IPIPSSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPHLL	100	B7	56.6	4
1147.05	pol 530	FPHCLAFSYM	95	B7	58.5	5
1039.06	env 359	WMMWYWGPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTFGRETVLEY	75	A1	80.0	3
1090.07	pol 415	LSLDVSAAFY	95	A1	6.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.07	core 117	EYLVSFGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3

FIG.21A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PADRE®
Core 141 A3
Pol 429 B7
Pol 149 A3
Env 183 A2
Pol 415 A1
Pol 745 A24
Env 332 A24
Pol 354 B7
Core 117 A24
Pol 538 A2
Core 419 A1
Pol 530 B7
Env 359 A1
Pol 531 A3
Pol 562 A2
Env 313 B7
Env 335 A2
Core 18 A2
Core 137 A1
Pol 665 A3
signal
Pol 538 A2
Core 117 A24
Core 419 A1
Pol 149 A3
Core 18 A2
Pol 530 B7
Env 332 A24
Pol 392 A24
Pol 665 A3
Pol 531 A3
Env 183 A2
Env 313 B7
Env 359 A1
Pol 354 B7
Pol 562 A2
Core 137 A1
Pol 429 B7
Core 141 A3
Env 335 A2
PADRE®
Pol 415 A1
Pol 745 A24

FIG.21B

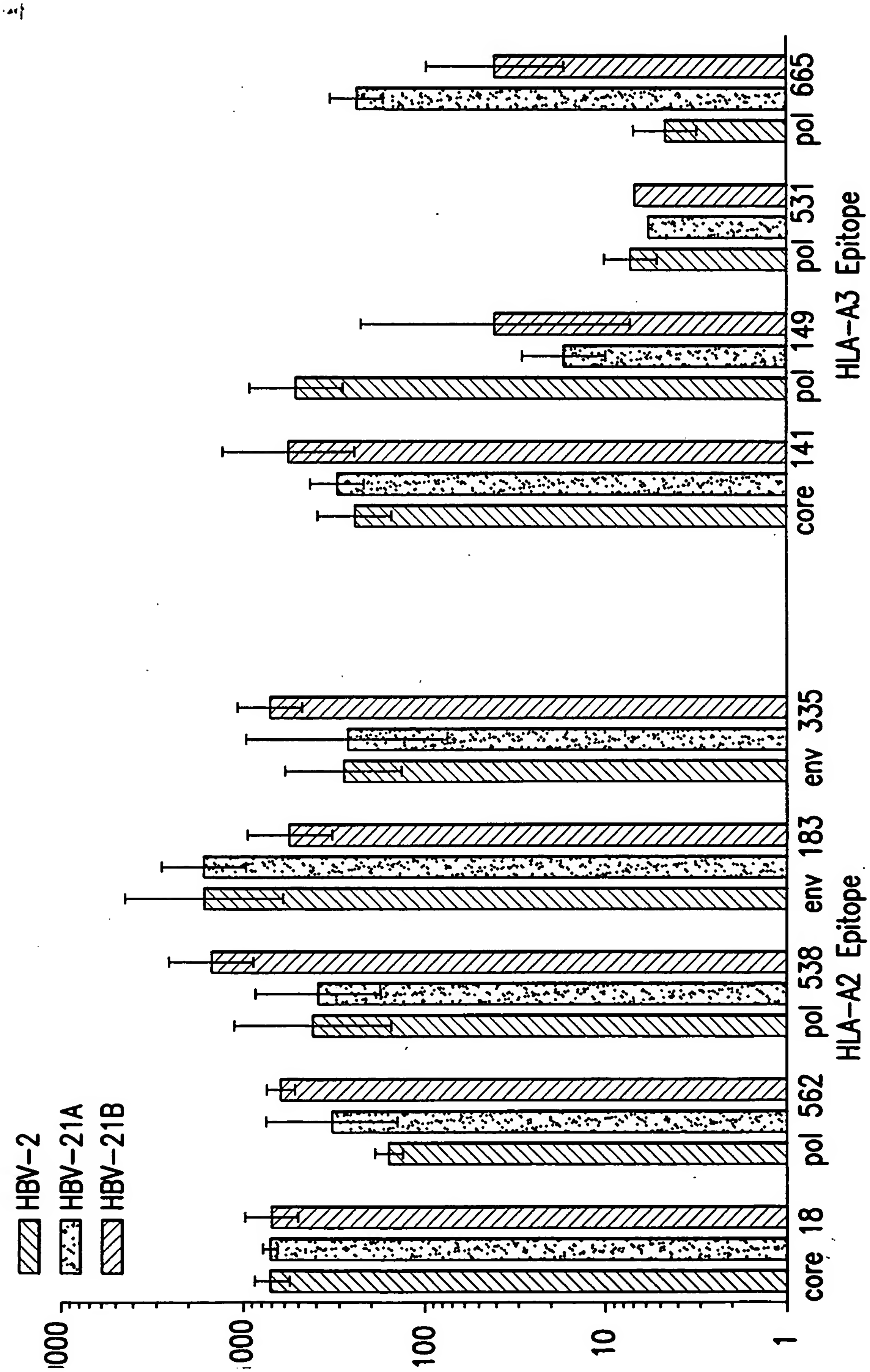
HBV-2
HBV-21A
HBV-21B
1000
1000
100
10
1
core 18
pol 562
pol 538
env 183
env 335
HLA-A2 Epitope
core 141
pol 149
pol 531
pol 665
HLA-A3 Epitope

FIG.21C

HBV-21A

MGMQVQIQSLFLLLLWVPGSRGSWPKFAVPNLKAAAAKFVAAWTLKAAAKSTLPETTVVRRKHPAAMPHLLKAAAHTL
WKAGILYKKAFLLTRILTIGALSLDVSAAFYNAAAKYTSFPWLLNAAARFSWLSLLVPFNAATPARVTGGVFKAAEYL
VSFGVWGAAAYMDDVVLGVNDLLDTASALYNAAAFPHCLAFSYMKAAAWMMWYWGPSLYKAASAICSVVRRKNFLLSL
GIHLNIPIPSSWAFKAAWLSLLVPFVNAFLPSDFFPSVKLTFGRETVLEYKQAFTFSPTYK

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATCTTGGCCTAAA
TTCGCAGTGCCAAACCTTAAAGCCGCGGCTGCTAAGTTCGTAGCTGCCTGGACACTAAAGGCCGCCGCTAAGAGCACA
CTGCCAGAGACCACCGTGGTCCGGCGAAAGCATCCAGCCGCAATGCCCCACTTGCTCAAAGCAGCCGCCCACACTCTT
TGGAAGGCTGGGATATTGTACAAGAAAGCCTTCCTTCTGACCAGGATATTAACTATCGGAGCTCTGTCACTCGACGTT
TCTGCTGCCTTCTACAACGCGGCGGCAAAATACACTAGCTTTCCATGGCTACTCAACGCAGCCGCCAGATTTTCTTGG
CTATCACTACTGGTGCCATTTAATGCAGCAACACCTGCTAGAGTGACTGGCGGCGTCTTTAAAGCAGCCGAGTACTTG
GTGAGCTTTGGCGTCTGGGGTGCAGCGGCATATATGGATGATGTAGTGTTAGGGGTGAACGACCTCCTGGACACAGCC
AGTGCGCTGTACAATGCAGCTGCATTCCCGCATTGCCTAGCCTTCAGTTATATGAAAGCAGCAGCCTGGATGATGTGG
TACTGGGGACCGTCCCTTTATAAAGCAGCTTCAGCAATCTGTTCCGTTGTGAGGAGAAAAAACTTTTTACTCTCCCTC
GGTATTCACCTGAACATTCCCATCCCTTCCTCATGGGCATTCAAAGCCGCTTGGCTGAGTCTACTCGTACCTTTCGTT
AATGCATTTCTGCCCAGCGACTTTTTCCCCTCGGTAAAACTGACATTCGGACGCGAAACAGTCCTTGAATATAAGCAG
GCCTTCACGTTCTCACCAACCTATAAATGA

FIG.21D

HBV-21B

MGMQVQIQSLFLLLLWVPGSRGYMDDVVLGVNAAAEYLVSFGVWNDLLDTASALYGAAHTLWKAGILYKKAFLPSDFF
PSVKAFPHCLAFSYMKAARFSWLSLLVPFNAASWPKFAVPNLKAAAQAFTFSPTYKNAAASAICSVVRRKAFLLTRIL
TINIPIPSSWAFKAAWMMWYWGPSLYKAAATPARVTGGVFKAANFLLSLGIHLNLTFGRETVLEYKHPAAMPHLLKAA
STLPETTVVRRKWLSLLVPFVNAAAAKFVAAWTLKAAAKLSLDVSAAFYNAAAKYTSFPWLL

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATACATGGATGAC
GTTGTGTTAGGCGTTAATGCAGCCGCAGAATATCTCGTGTCATTCGGCGTCTGGAACGACCTGTTGGACACTGCATCT
GCTCTGTACGGTGCAGCCCATACCCTGTGGAAGGCCGGAATCCTCTACAAAAAGGCATTCCTACCTAGCGACTTTTTT
CCTTCAGTGAAAGCCTTCCCACATTGCCTAGCATTCTCGTATATGAAAGCGGCTAGGTTCTCATGGCTTAGTCTTCTA
GTACCTTTCAATGCCGCCTCCTGGCCCAAATTCGCCGTACCAAATCTAAAAGCGGCCGCGCAGGCCTTTACATTCTCT
CCGACTTATAAAAATGCAGCAGCCTCCGCTATTTGTAGCGTCGTGCGCCGAAAGGCCTTCCTGCTAACCCGGATTTTG
ACGATAAACATCCCCATCCCTTCTAGCTGGGCTTTCAAAGCAGCATGGATGATGTGGTACTGGGGTCCCAGCTTATAC
AAAGCTGCGGCAACCCCAGCAAGAGTGACAGGGGGCGTGTTTAAGGCCGCCAACTTCCTCCTGAGTCTCGGAATACAC
CTGAACTTAACCTTTGGGAGAGAGACAGTACTGGAGTATAAACACCCAGCAGCTATGCCGCACCTACTCAAAGCCGCT
TCAACACTCCCAGAAACAACTGTAGTGAGGAGAAAATGGCTCTCCCTGCTTGTCCCATTTGTCAACGCCGCCGCCGCT
AAGTTTGTGGCCGCTTGGACACTTAAGGCTGCAGCAAAGTTGTCACTTGATGTTAGTGCAGCGTTCTATAACGCAGCT
GCAAAATACACTTCCTTTCCCTGGCTGCTGTGA

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN
924.07	core 18	FLPSDFFPSV	45	A2	3.5	5
777.03	env 183	FLLTRILTI	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
1168.02	pol 455	GLSRYVARL	55	A2	55.9	3
1090.77	pol 538	YMDDVVLGV	90	A2/A1	6.4	5
927.11	pol 562	FLLSLGIHL	95	A2	7.8	3
1083.01	core 141	STLPETTVVRR	95	A3/A11	735/4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4/15.6	5
1069.20	pol 388	LVVDFSQFSR	100	A3/A11	6875/17	3
1069.16	pol 47	NVSIPWTHK	100	A3/A11	174/117	3
1090.11	pol 531	SAICSVVRR	95	A3/A11	2189/29	3
1090.10	pol 665	QAFTFSPTYK	95	A3/A11	249/8	3
988.05	core 19	LPSDFFPSV	45	B7	3026.8	4
1145.04	env 313	IPIPSSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPHLL	100	B7	56.6	4
1147.05	pol 530	FPHCLAFSYM	95	B7	58.5	5
1359.01	pol 640	YPALMPLYACI	95	B7	1393.4	3
1039.06	env 359	WMMWYWGPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTFGRETVLEY	75	A1	80.0	3
1373.78	pol 166	ASFCGSPY	100	A1	247.0	3
1090.07	pol 415	LSLDVSAAFY	95	A1	6.0	3
1069.08	env 249	ILLLCLIFLL	100	A1	192.0	1
20.0269	env 236	RWMCLRRFII	95	A24	11.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.38	core 101	LWFHISCLTF	85	A24	6.7	3
1373.07	core 117	EYLVSFGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3

FIG.22A

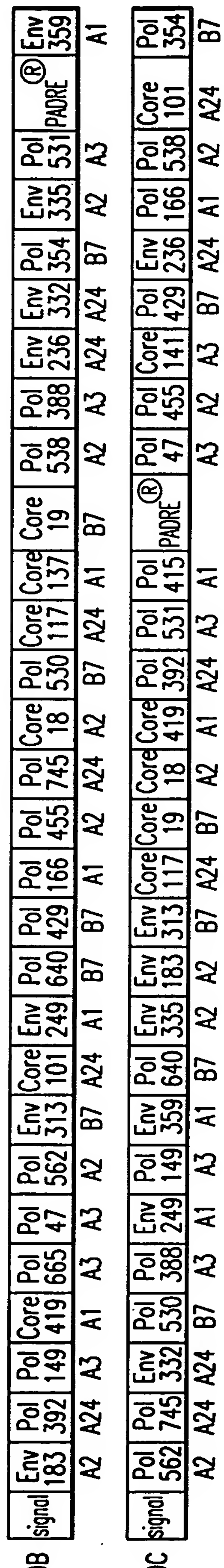
B
signal
Env 183 A2
Pol 392 A24
Pol 149 A3
Core 419 A1
Pol 665 A3
Pol 47 A3
Pol 562 A2
Env 313 B7
Core 101 A24
Env 249 A1
Pol 640 B7
Pol 429 B7
Pol 166 A1
Pol 455 A2
Pol 745 A24
Core 18 A2
Pol 530 B7
Core 117 A24
Core 137 A1
Core 19 B7
Pol 538 A2
Pol 388 A3
Env 236 A24
Env 332 A24
Pol 354 B7
Env 335 A2
Pol 531 A3
PADRE®
Env 359 A1
C
signal
Pol 562 A2
Pol 745 A24
Env 332 A24
Pol 530 B7
Pol 388 A3
Env 249 A1
Pol 149 A3
Env 359 A1
Pol 640 B7
Env 335 A2
Env 183 A2
Env 313 B7
Core 117 A24
Core 19 B7
Core 18 A2
Core 419 A1
Pol 392 A24
Pol 531 A3
Pol 415 A1
PADRE®
Pol 47 A3
Pol 455 A2
Core 141 A3
Pol 429 B7
Env 236 A24
Pol 166 A1
Pol 538 A2
Core 101 A24
Pol 354 B7

FIG.22B

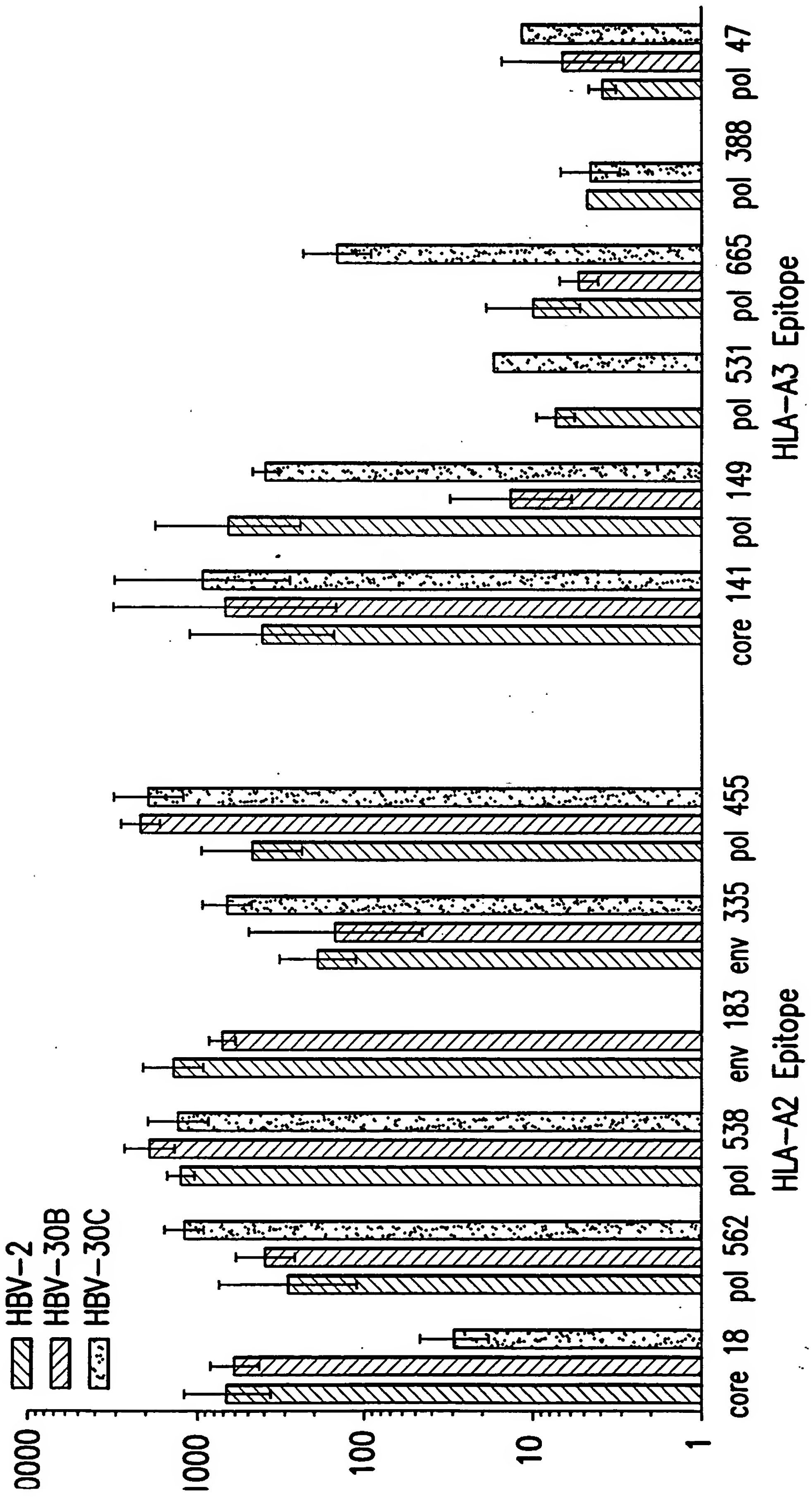
HBV-2
HBV-30B
HBV-30C
0000
1000
100
10
1
core 18
pol 562
pol 538
env 183
env 335
pol 455
HLA-A2 Epitope
core 141
pol 149
pol 531
pol 665
pol 388
pol 47
HLA-A3 Epitope

FIG.22C

HBV-30B

MGMQVQIQSLFLLLLWVPGSRGFLLTRILTINAAASWPKFAVPNLKAAAHTLWKAGILYKKADLLDTASALYNQAFTFS
PTYKGAAANVSIPWTHKGAAAFLLSLGIHLNIPIPSSWAFKAAALWFHISCLTFKAAAILLLCLIFLLNAAAYPALMPL
YACINAHPAAMPHLLKAAASFCGSPYKAAGLSRYVARLNKYTSFPWLLNFLPSDFFPSVKAFPHCLAFSYMKAEYLVSF
GVWNAALTFGRETVLEYKAAALPSDFFPSVKAYMDDVVLGVNLVVDFSQFSRNAAARWMCLRRFIINAARFSWLSLLVP
FNAATPARVTGGVFKAAWLSLLVPFVNSAICSVVRRKAKFVAAWTLKAAAKWMMWYWGPSLYKAASTLPETTVVRRKLS
LDVSAAFY

ATGGGAATGCAGGTCCAGATACAGAGCTTGTTCCTCCTCCTGCTTTGGGTCCCCGGATCAAGGGGTTTCCTCCTAACCC
GCATCCTGACAATTAACGCCGCAGCCTCCTGGCCAAAATTTGCCGTGCCAAATCTCAAGGCAGCTGCACACACACTATG
GAAAGCAGGGATACTGTACAAGAAAGCCGATCTGCTAGACACAGCGTCTGCGTTGTACAACCAGGCTTTTACTTTCTCT
CCTACATATAAAGGCGCAGCTGCAAACGTGAGTATCCCTTGGACGCACAAAGGAGCCGCTGCCAACTTCTTACTGTCCC
TGGGCATCCATCTAAATATCCCTATTCCTTCATCCTGGGCATTTAAAGCAGCCGCCTTATGGTTCCACATAAGTTGTCT
GACCTTCAAAGCCGCAGCAATCCTGCTCCTTTGCCTCATTTTCTTACTAAACGCCGCTGCCTATCCAGCTCTTATGCCA
TTGTACGCATGTATCAACGCCCACCCCGCAGCAATGCCCCACCTCCTTAAAGCTGCCGCCAGTTTCTGCGGTTCTCCTT
ATAAAGCAGCAGGGCTGTCCAGATACGTAGCTAGGCTAAACAAGTATACCAGCTTCCCCTGGTTACTTAATTTCCTGCC
GTCAGATTTCTTTCCATCAGTTAAGGCCTTCCCTCATTGTCTGGCCTTTAGCTACATGAAGGCTGAATATTTGGTATCC
TTCGGCGTGTGGAATGCGGCACTGACATTTGGAAGGGAGACAGTGCTCGAGTACAAAGCCGCCGCACTACCCTCGGACT
TCTTCCCATCGGTCAAAGCTTACATGGACGATGTAGTCCTCGGCGTTAACTTAGTAGTGGACTTTTCTCAATTTTCCAG
AAACGCAGCGGCCAGATGGATGTGCCTTCGGCGTTTTATAATAAACGCCGCTCGATTCAGCTGGCTATCACTCCTAGTT
CCATTTAATGCAGCTACACCCGCACGGGTGACAGGTGGAGTTTTCAAGGCAGCGTGGCTTTCACTGCTTGTGCCATTTG
TGAACTCAGCTATTTGCTCAGTAGTGAGAAGGAAGGCAAAATTCGTCGCTGCCTGGACTCTCAAAGCTGCCGCAAAGTG
GATGATGTGGTATTGGGGACCGAGCTTGTACAAAGCGGCCTCTACTCTGCCAGAAACTACCGTAGTGAGAAGAAAACTG
AGCCTGGACGTCAGCGCGGCATTCTACTGA

FIG.22D

HBV-30C

MGMQVQIQSLFLLLLWVPGSRGFLLSLGIHLNAAAKYTSFPWLLNAAARFSWLSLLVPFNAAFPHCLAFSYMKAALVVD
FSQFSRGAILLLLCLIFLLNAAAHTLWKAGILYKKAWMMWYWGPSLYKAYPALMPLYACIGAAAWLSLLVPFVNFLLTRI
LTINIPIPSSWAFKAAAEYLVSFGVWNLPSDFFPSVKFLPSDFFPSVKDLLDTASALYNSWPKFAVPNLKAAASAICSV
VRRKLSLDVSAAFYNAAAKFVAAWTLKAAAKAANVSIPWTHKGAAGLSRYVARLNAAASTLPETTVVRRKHPAAMPHLL
KAAARWMCLRRFIINASFCGSPYKAAYMDDVVLGVNALWFHISCLTFKAAATPARVTGGVFKAAALTFGRETVLEYKQA
FTFSPTYK

ATGGGAATGCAGGTGCAAATACAGTCTCTCTTCCTTTTGCTTCTCTGGGTTCCAGGATCACGGGGCTTCTTGCTTAGCT
TGGGCATCCACCTAAATGCTGCTGCAAAATACACATCTTTTCCTTGGCTCCTTAATGCCGCCGCTAGGTTTTCATGGCT
GAGTCTGCTAGTACCTTTCAATGCGGCTTTCCCACATTGCCTAGCTTTTAGCTATATGAAAGCTGCTTTAGTCGTGGAC
TTTTCACAGTTTAGCAGAGGAGCAATCCTGCTGCTATGTCTGATATTCCTTCTAAACGCAGCAGCCCACACACTCTGGA
AAGCTGGTATCCTTTACAAGAAAGCCTGGATGATGTGGTATTGGGGACCCAGCCTCTACAAAGCATACCCTGCCCTGAT
GCCACTATACGCATGCATTGGCGCGGCAGCCTGGTTATCCCTTTTAGTACCGTTTGTCAACTTTCTATTAACCAGAATC
CTGACGATTAATATTCCGATCCCAAGTTCCTGGGCATTCAAAGCAGCCGCGGAGTATCTGGTTTCATTTGGCGTATGGA
ACCTGCCAAGCGACTTCTTTCCTTCTGTTAAGTTCCTCCCCTCCGATTTCTTTCCATCGGTGAAAGACCTCCTTGATAC
CGCGAGCGCTCTGTACAACTCGTGGCCAAAATTCGCAGTTCCAAACCTAAAAGCCGCCGCCAGTGCCATTTGTTCCGTG
GTAAGGAGAAAATTATCACTCGACGTGTCCGCAGCATTTTATAACGCTGCTGCAAAGTTTGTCGCAGCATGGACATTGA
AGGCTGCAGCGAAAGCAGCAAATGTATCAATACCCTGGACCCACAAGGGTGCAGCCGGGCTGTCTAGGTATGTGGCGAG
GCTAAACGCCGCCGCCTCAACACTGCCTGAGACTACTGTCGTGAGACGCAAACACCCTGCCGCAATGCCCCACCTGCTG
AAAGCAGCCGCACGATGGATGTGCCTCAGAAGATTCATAATAAACGCTTCTTTCTGTGGGTCACCCTACAAAGCCGCTT
ACATGGACGATGTGGTCCTCGGAGTGAATGCCCTCTGGTTCCATATCAGCTGCCTGACATTCAAGGCAGCCGCCACCCC
CGCTCGTGTGACAGGAGGTGTCTTCAAAGCCGCGGCACTGACTTTCGGTCGGGAAACTGTATTGGAATATAAGCAGGCC
TTCACATTCTCCCCAACATACAAGTGA

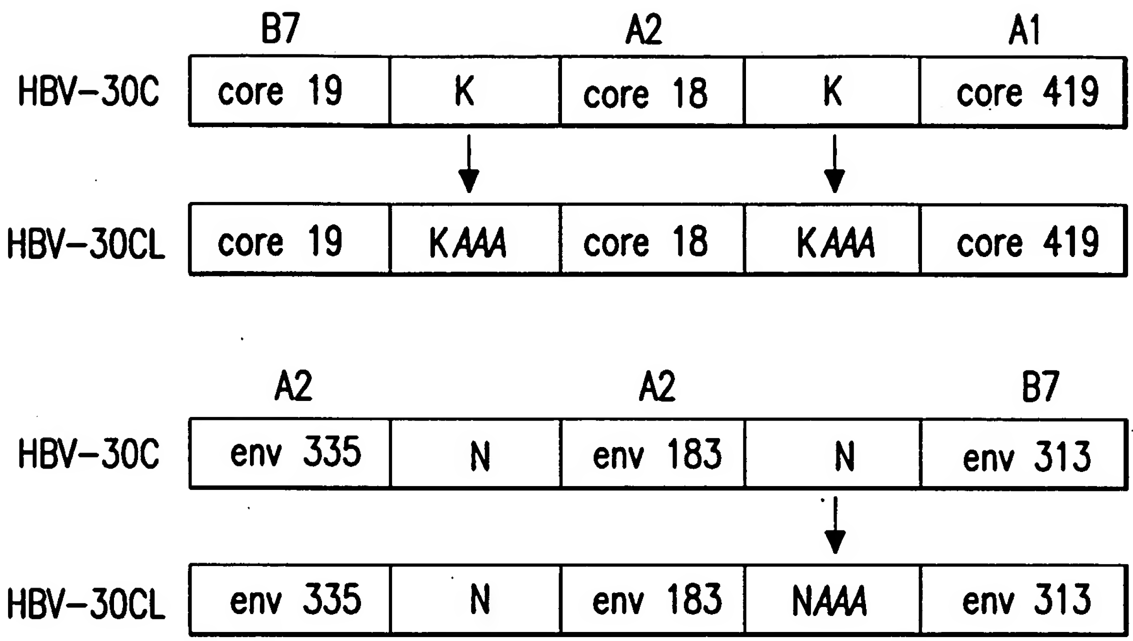
B7
A2
A1
HBV-30C
core 19
K
core 18
K
core 419
HBV-30CL
core 19
KAAA
core 18
KAAA
core 419
A2
A2
B7
HBV-30C
env 335
N
env 183
N
env 313
HBV-30CL
env 335
N
env 183
NAAA
env 313

FIG.23A

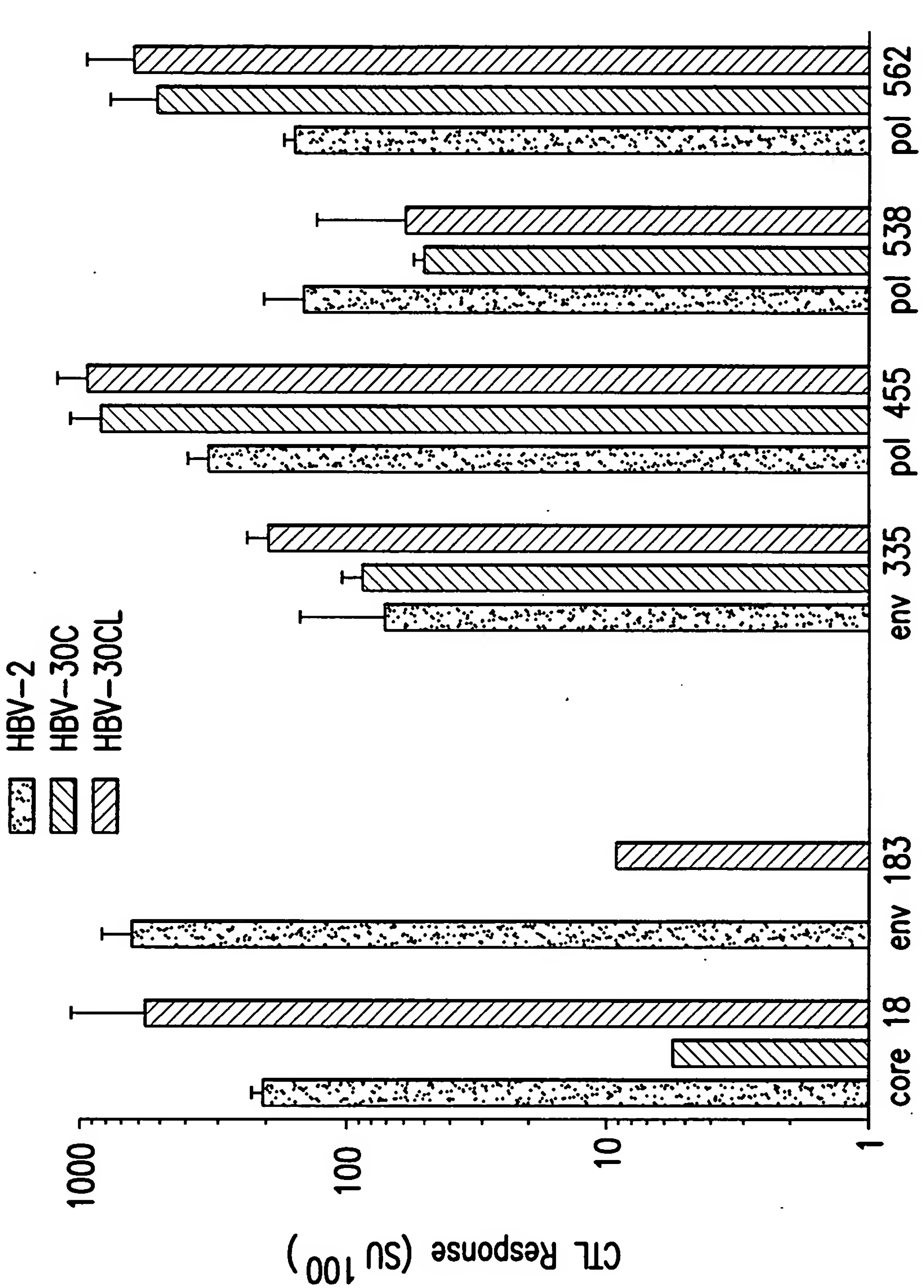
HBV-2
HBV-30C
HBV-30CL
CTL Response (SU 100)
1000
100
10
1
core 18
env 183
env 335
pol 455
pol 538
pol 562

FIG.23B

HBV-CL

MQVQIQSLFLLLLWVPGSRGFLLSLGIHLNAAAKYTSFPWLLNAAARFSWLSLLVPFNAAFPHCLAFSYMKA
ALVVDFSQFSRGAILLLCLIFLLNAAAHTLWKAGILYKKAWMMWYWGPSLYKAYPALMPLYACIGAAAWLSL
LVPFVNFLLTRILTINAAAIPIPSSWAFKAAAEYLVSFGVWNLPSDFFPSVKAAAFLPSDFFPSVKAAADLL
DTASALYNSWPKFAVPNLKAAASAICSVVRRKLSLDVSAAFYNAAAKFVAAWTLKAAAKAANVSIPWTHKGA
AGLSRYVARLNAAASTLPETTVVRRKHPAAMPHLLKAAARWMCLRRFIINASFCGSPYKAAYMDDVVLGVNA
LWFHISCLTFKAAATPARVTGGVFKAAALTFGRETVLEYKQAFTFSPTYK

ATGGGAATGCAGGTGCAAATACAGTCTCTCTTCCTTTTGCTTCTCTGGGTTCCAGGATCACGGGGCTTCTTG
CTTAGCTTGGGCATCCACCTAAATGCTGCTGCAAAATACACATCTTTTCCTTGGCTCCTTAATGCCGCCGCT
AGGTTTTCATGGCTGAGTCTGCTAGTACCTTTCAATGCGGCTTTCCCACATTGCCTAGCTTTTAGCTATATG
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CTAAACGCAGCAGCCCACACACTCTGGAAAGCTGGTATCCTTTACAAGAAAGCCTGGATGATGTGGTATTGG
GGACCCAGCCTCTACAAAGCATACCCTGCCCTGATGCCACTATACGCATGCATTGGCGCGGCAGCCTGGTTA
TCCCTTTTAGTACCGTTTGTCAACTTTCTATTAACCAGAATCCTGACGATTAATGCTGCCGCCATTCCGATC
CCAAGTTCCTGGGCATTCAAAGCAGCCGCGGAGTATCTGGTTTCATTTGGCGTATGGAACCTGCCAAGCGAC
TTCTTTCCTTCTGTTAAGGCCGCTGCTTTCCTCCCCTCCGATTTCTTTCCATCGGTGAAAGCCGCTGCCGAC
CTCCTTGATACCGCGAGCGCTCTGTACAACTCGTGGCCAAAATTCGCAGTTCCAAACCTAAAAGCCGCCGCC
AGTGCCATTTGTTCCGTGGTAAGGAGAAAATTATCACTCGACGTGTCCGCAGCATTTTATAACGCTGCTGCA
AAGTTTGTCGCAGCATGGACATTGAAGGCTGCAGCGAAAGCAGCAAATGTATCAATACCCTGGACCCACAAG
GGTGCAGCCGGGCTGTCTAGGTATGTGGCGAGGCTAAACGCCGCCGCCTCAACACTGCCTGAGACTACTGTC
GTGAGACGCAAACACCCTGCCGCAATGCCCCACCTGCTGAAAGCAGCCGCACGATGGATGTGCCTCAGAAGA
TTCATAATAAACGCTTCTTTCTGTGGGTCACCCTACAAAGCCGCTTACATGGACGATGTGGTCCTCGGAGTG
AATGCCCTCTGGTTCCATATCAGCTGCCTGACATTCAAGGCAGCCGCCACCCCCGCTCGTGTGACAGGAGGT
GTCTTCAAAGCCGCGGCACTGACTTTCGGTCGGGAAACTGTATTGGAATATAAGCAGGCCTTCACATTCTCC
CCAACATACAAGTGA

FIG.23C

Epitope	# DR Bound	HLA-DR Binding Capacity (IC50 nM)													
		DRB1*0101	DRB1*1501	DRB1*0301	DRB1*0401	DRB1*0405	DRB1*1101	DRB1*1201	DRB1*1302	DRB1*0701	DRB1*0802	DRB1*0901	DRB5*0101	DRB3*0101	DRB4*0101
pol 412	10	2.0	21	-	10.0	47	303	397	143	173	598	791	1067	1837	4179
pol 664	11	10	41	-	88	181	82	-	190	90	416	142	144	4848	322
env 180	10	1	217	-	9	258	6	4229	9	8	189	56	1158	4374	696
pol 774	9	15	748	-	119	94	443	-	-	94	818	220	400	-	-
core 120	8	27	43	-	58	220	11	817	565	78	76	1773	7	6454	395
pol 145	10	17	4.0	-	2271	1499	42	149	766	61	36	133	35	-	782
env 339	9	408	14	-	315	28	54	452	2330	2744	60	31	1516	1661	22
pol 501	8	248	558	-	77	244	492	9462	-	-	800	1551	560	-	102
pol 523	7	27	359	-	560	246	1749	-	59	328	940	1373	4764	-	1347
pol 618	6	3.0	4370	-	40	34	1617	-	821	62	872	5175	1246	-	3060
pol 767	8	55	386	-	966	1634	1520	802	143	44	214	299	3276	-	6553
core 50	7	810	8.0	-	326	-	458	-	-	676	210	952	124	575	48
pol 694	2	7470	5009	67	490	1203	-	-	2022	-	-	-	-	1808	1044
pol 385	3	7372	1368	36	208	251	-	-	946	-	-	-	-	2525	8711
pol 96	1	8415	4153	43	3916	1908	6666	-	4461	-	5354	-	4330	-	8121
pol 420	4	38	3089	62	168	17	4923	1859	36	5063	1065	7126	-	5	7

FIG.24A

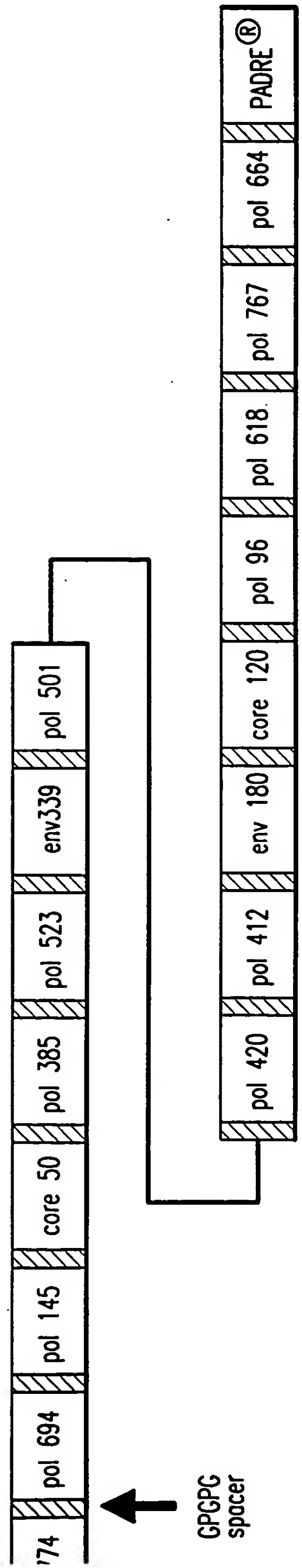

PADRE®
pol 664
pol 767
pol 618
pol 96
core 120
env 180
pol 412
pol 420
pol 501
env339
pol 523
pol 385
core 50
pol 145
pol 694
'74
GPGPG spacer

FIG.24B

HBV-HTL

MGTSFVYVPSALNPADGPGPGLCQVFADATPTGWGLGPGPGRHYLHTLWKAGILYKGPGPGPHHTALRQAILC
WGELMTLAGPGPGESRLVVDFSQFSRGNGPGPGPFLLAQFTSAICSVVGPGPGLVPFVQWFVGLSPTVGPGPG
LHLYSHPIILGFRKIGPGPGSSNLSWLSLDVSAAFGPGPGLQSLTNLLSSNLSWLGPGPGAGFFLLTRILTIP
QSGPGPGVSFGVWIRTPPAYRPPNAPIGPGPGVGPLTVNEKRRLKLIGPGPGKQCFRKLPVNRPIDWGPGPGA
ANWILRGTSFVYVPGPGPGKQAFTFSPTYKAFLCGPGPGAKFVAAWTLKAAA

ATGGGAACTTCTTTTGTGTATGTCCCTTCCGCTCTGAACCCAGCAGACGGACCCGGGCCTGGCCTGTGCCAGG
TCTTCGCCGACGCAACTCCCACAGGGTGGGGGCTGGGGCCAGGACCAGGCAGGCACTACCTGCATACTCTGTG
GAAGGCAGGAATCCTCTATAAAGGGCCCGGCCCAGGCCCTCACCACACCGCCCTGAGGCAGGCCATCCTGTGC
TGGGGGGAGCTCATGACCCTGGCCGGACCTGGACCCGGGGAGAGCAGACTGGTGGTGGATTTCAGCCAATTCA
GCAGAGGAAACGGACCCGGCCCTGGGCCTTTTCTGCTGGCTCAGTTTACATCTGCTATTTGTTCTGTGGTCGG
CCCCGGGCCCGGACTCGTGCCTTTCGTGCAGTGGTTCGTGGGACTGTCCCCTACAGTCGGGCCCGGCCCAGGG
CTGCATCTGTACTCCCACCCAATCATCCTCGGCTTCCGCAAGATTGGACCCGGCCCAGGCTCCAGCAATCTCT
CCTGGCTCTCTCTGGACGTGTCTGCCGCCTTTGGCCCTGGACCAGGCCTGCAAAGCCTGACTAATCTGCTCAG
CAGCAACCTGTCCTGGCTGGGACCTGGCCCAGGGGCTGGCTTCTTTCTGCTCACCCGGATTCTCACAATTCCC
CAGTCCGGACCAGGACCAGGAGTCAGTTTCGGGGTGTGGATCAGGACCCCTCCTGCTTATAGACCACCCAATG
CTCCAATCGGCCCCGGCCCTGGCGTCGGGCCACTGACCGTGAATGAGAAGCGCCGGCTGAAGCTGATCGGCCC
TGGCCCTGGCAAGCAGTGCTTTCGCAAACTGCCCGTGAACAGACCTATTGATTGGGGCCCCGGCCCTGGAGCA
GCCAACTGGATTCTCAGGGGAACAAGCTTCGTCTACGTGCCCGGGCCCGGACCAGGGAAGCAGGCTTTTACCT
TCTCTCCCACTTACAAGGCCTTCCTCTGTGGGCCAGGCCCCGGCGCCAAGTTTGTGGCAGCATGGACCCTCAA
AGCCGCTGCCTGA

FIG.24C

Appl. No. 10/677,754; Filed: Oct 3, 2003
Dkt No. 2060.0200003/HCC/PAC; Group Unit: To be assigned
Inventors: SETTE et al.
Tel. No.: 202-371-2600
For: Optimized Multi-Epitope Constructs and Uses Thereof

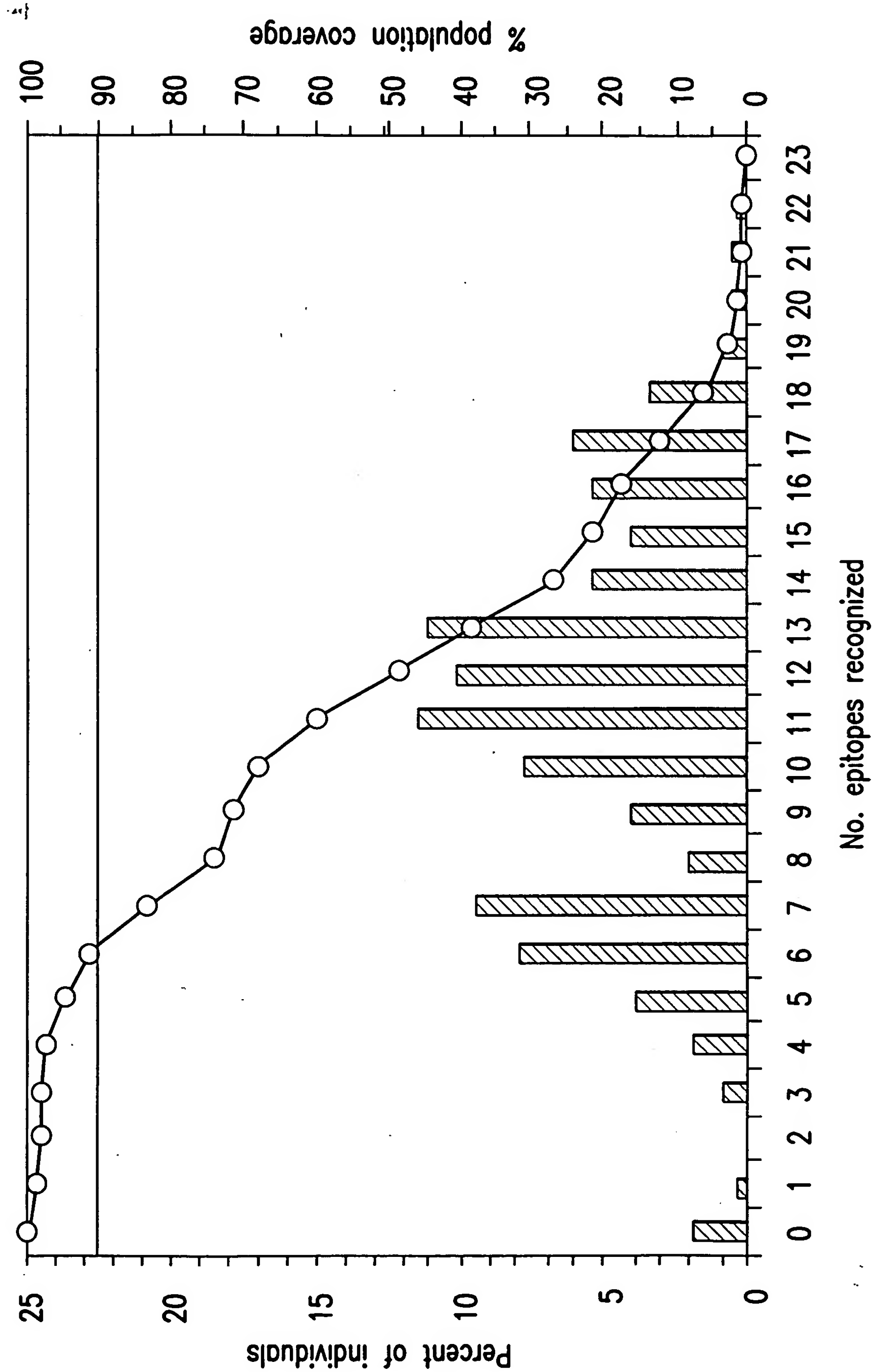


FIG.25A

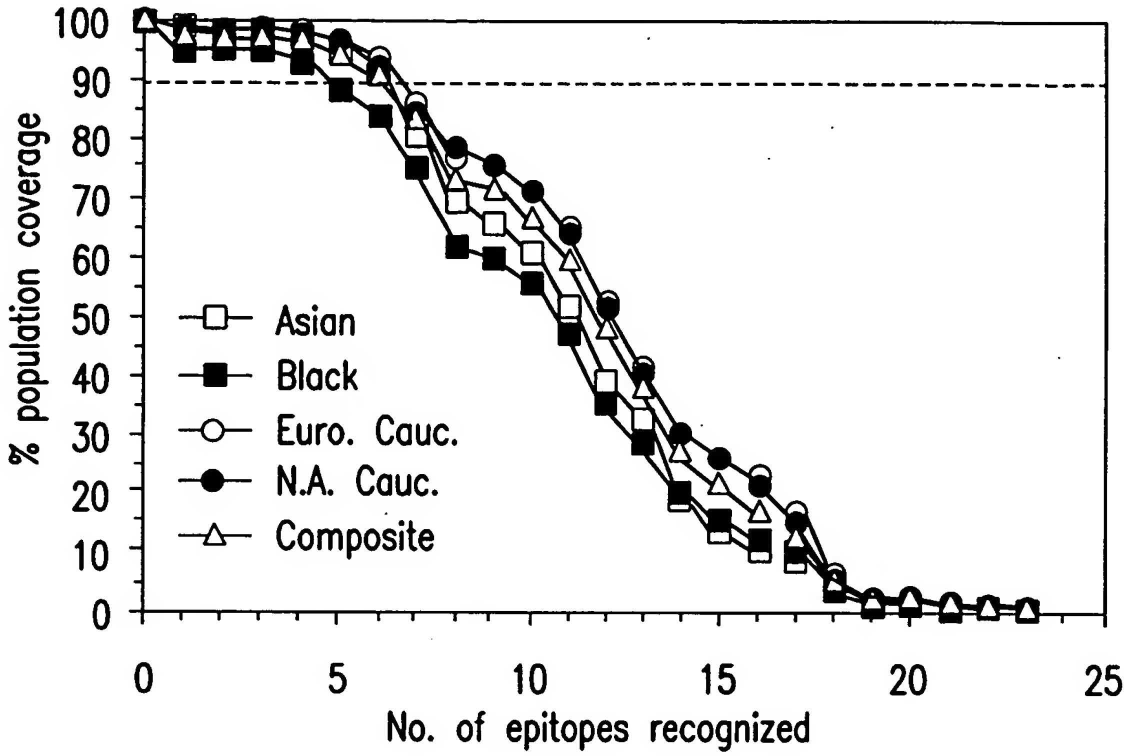

100
90
80
70
60
50
40
30
20
10
0
% population coverage
0
5
10
15
20
25
No. of epitopes recognized
Asian
Black
Euro. Cauc.
N.A. Cauc.
Composite

FIG.25B

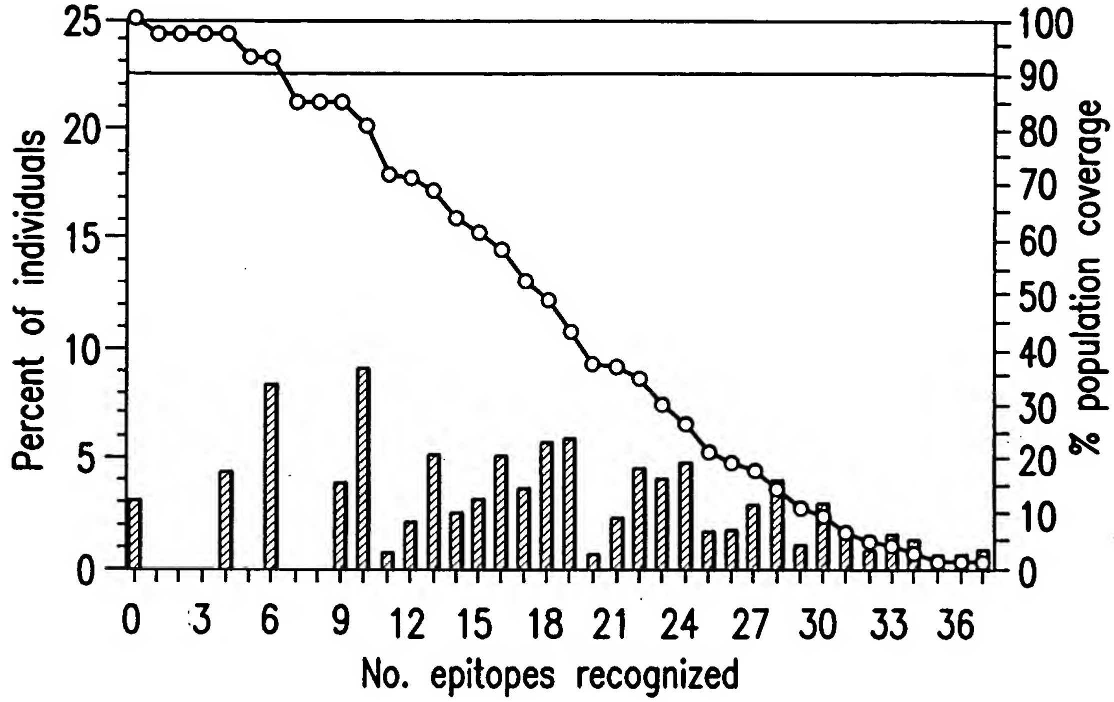


FIG.26A

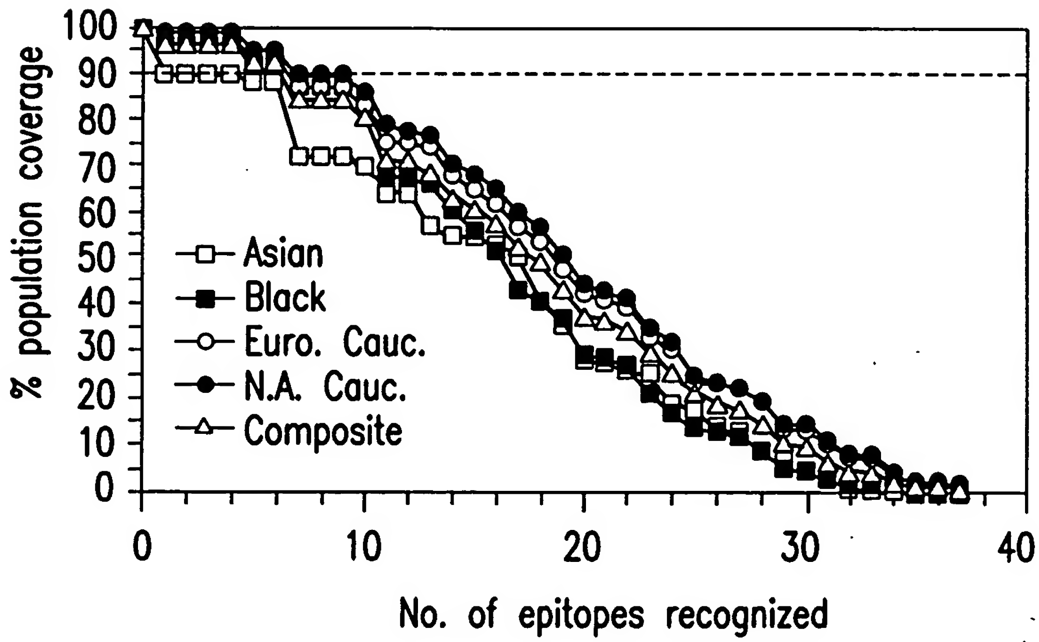


FIG.26B

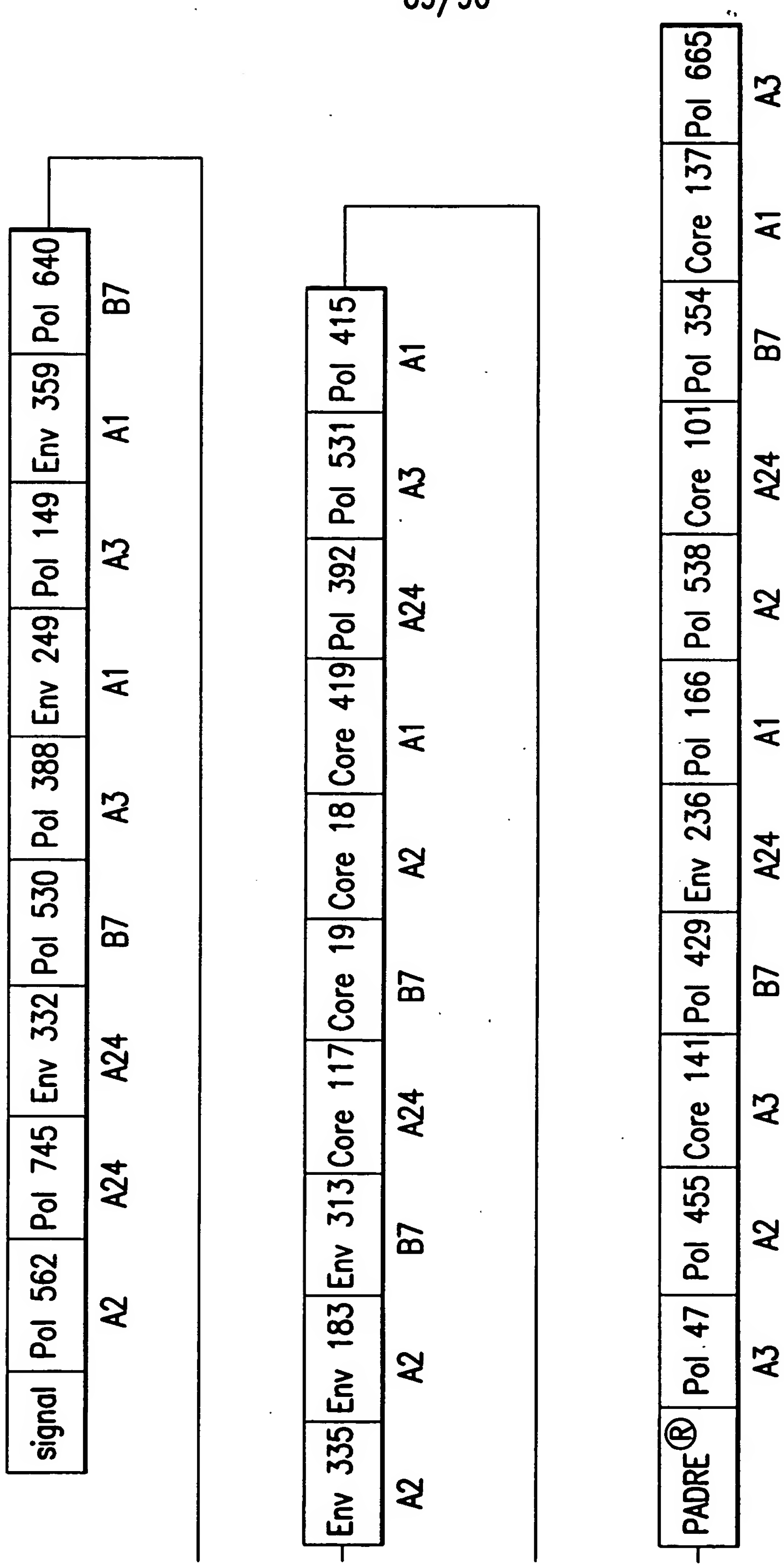

signal
Pol 562
A2
Pol 745
A24
Env 332
A24
Pol 530
B7
Pol 388
A3
Env 249
A1
Pol 149
A3
Env 359
A1
Pol 640
B7
Env 335
A2
Env 183
A2
Env 313
B7
Core 117
A24
Core 19
B7
Core 18
A2
Core 419
A1
Pol 392
A24
Pol 531
A3
Pol 415
A1
PADRE®
Pol 47
A3
Pol 455
A2
Core 141
A3
Pol 429
B7
Env 236
A24
Pol 166
A1
Pol 538
A2
Core 101
A24
Pol 354
B7
Core 137
A1
Pol 665
A3

FIG.27A

Appl. No. 10/677,754; Filed: Oct 3, 2003
Dkt No. 2060.0200003/HCC/PAC; Group Unit: To be assigned
Inventors: SETTE et al.
Tel. No.: 202-371-2600
For: Optimized Multi-Epitope Constructs and Uses Thereof

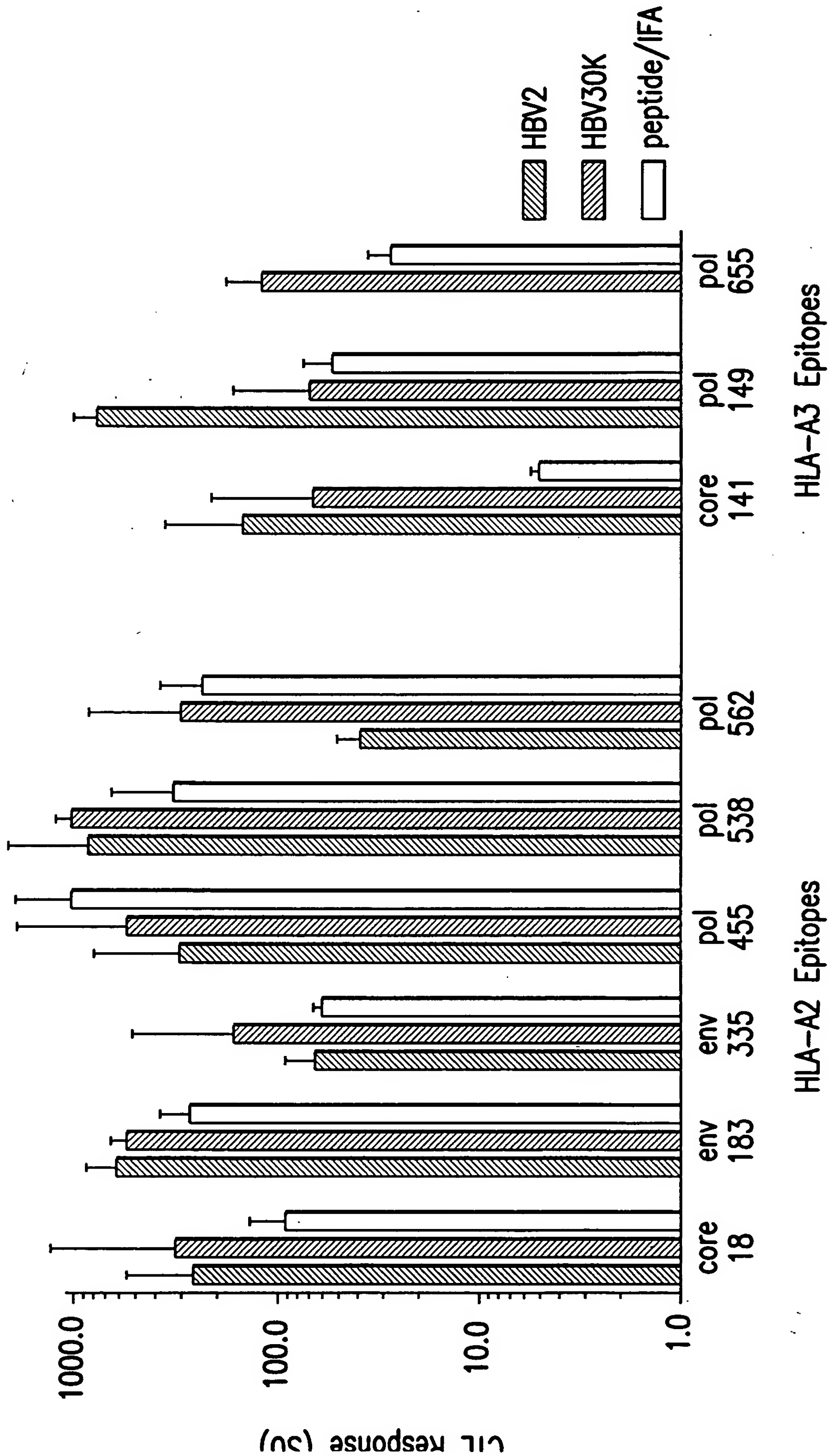


FIG.27B

Appl. No. 10/677,754; Filed: Oct 3, 2003
Dkt No. 2060.0200003/HCC/PAC; Group Unit: To be assigned
Inventors: SETTE et al.
Tel. No.: 202-371-2600
For: Optimized Multi-Epitope Constructs and Uses Thereof

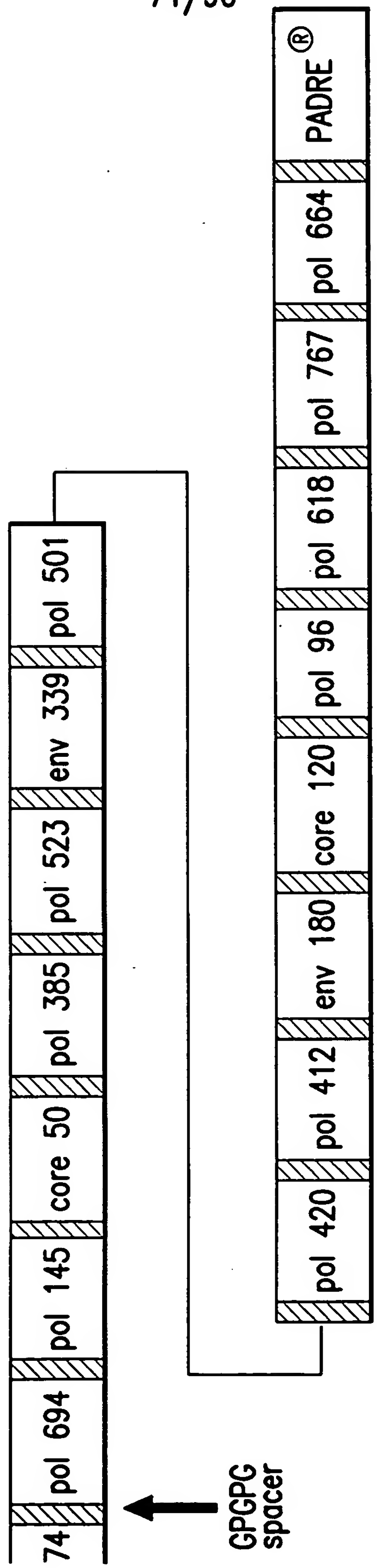


FIG.28A

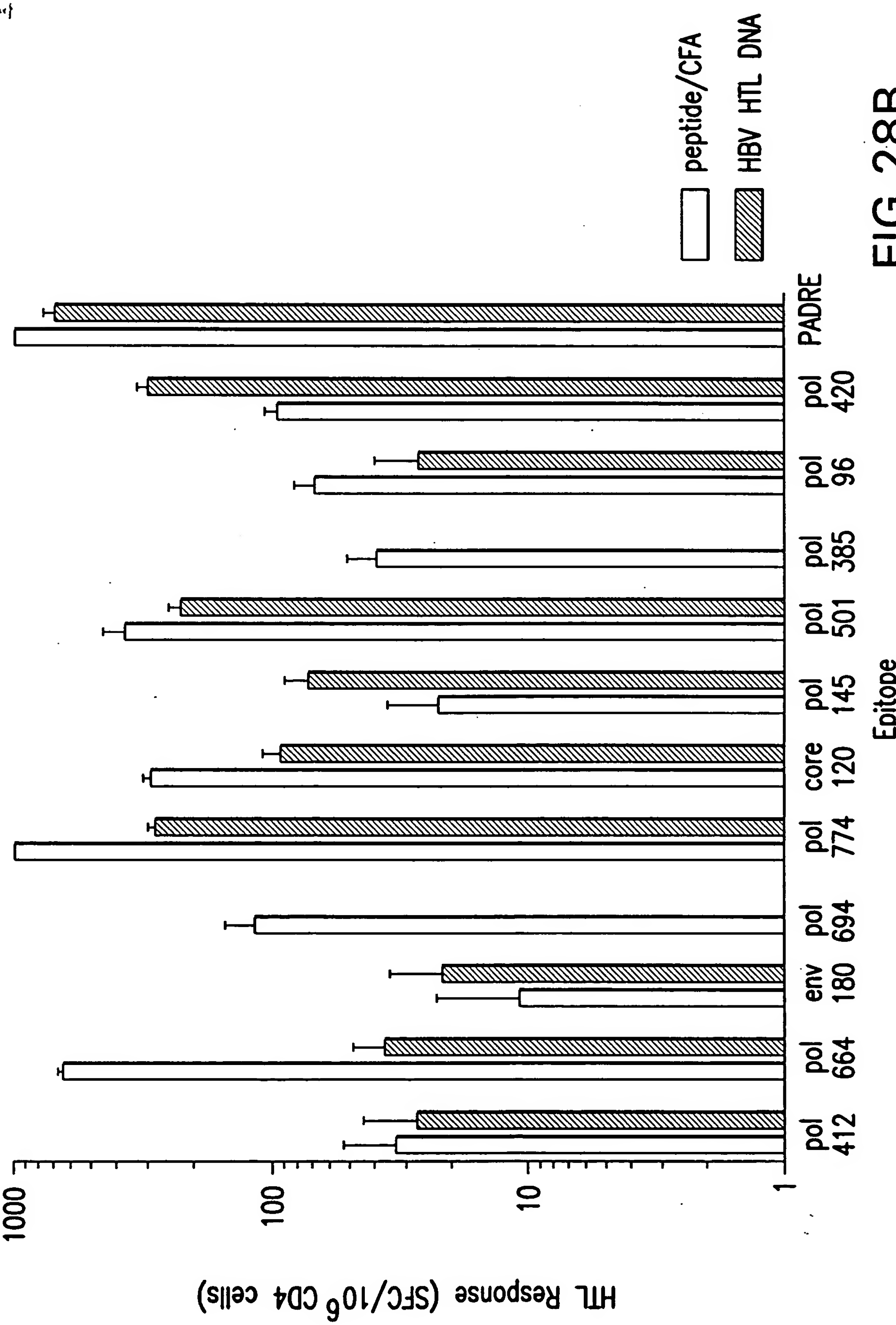

peptide/CFA
HBV HTL DNA
HTL Response (SFC/10^6 CD4 cells)
1000
100
10
1
Epitope
pol 412
pol 664
env 180
pol 694
pol 774
core 120
pol 145
pol 501
pol 385
pol 96
pol 420
PADRE

FIG.28B

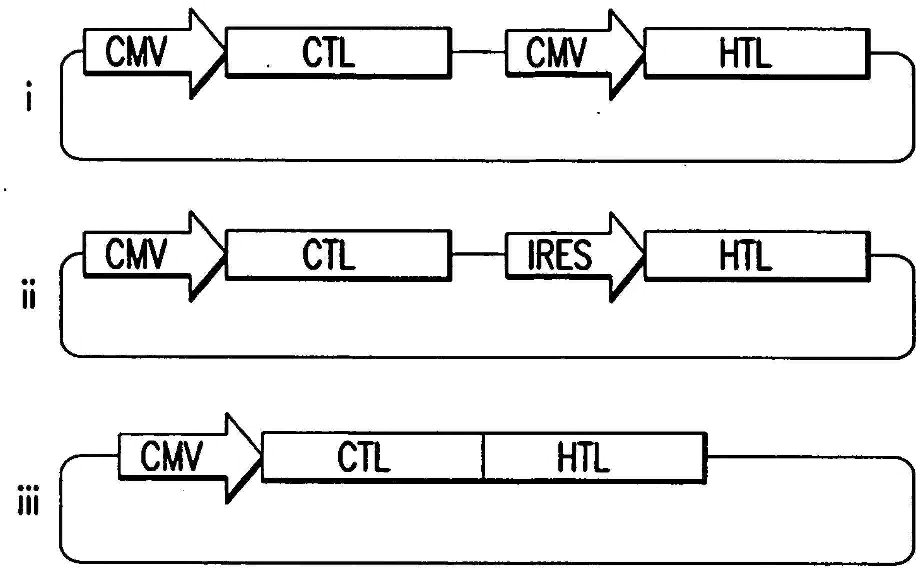
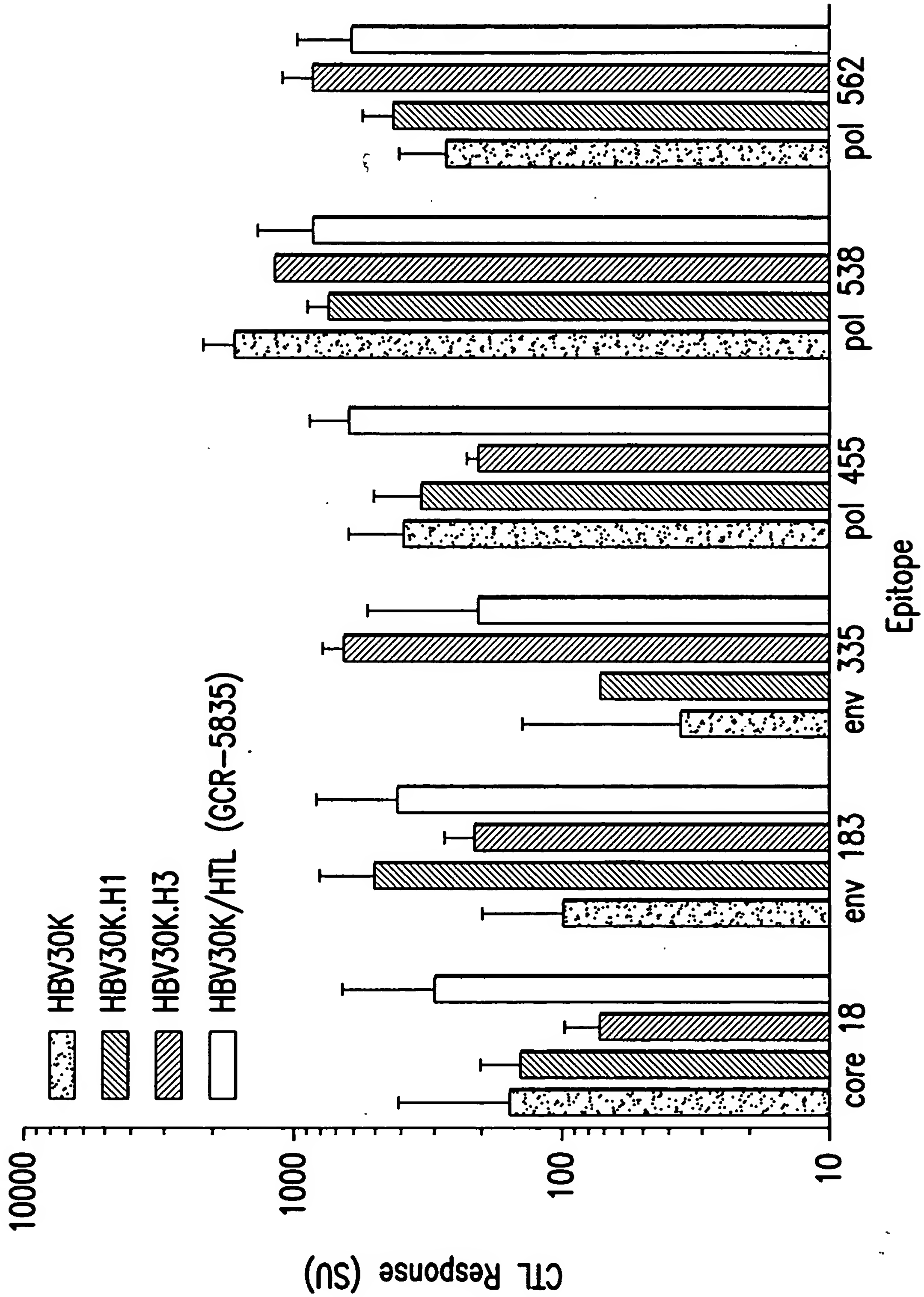


FIG.29A



HBV30K
HBV30K.H1
HBV30K.H3
HBV30K/HTL (GCR-5835)
CTL Response (SU)
10000
1000
100
10
core 18
env 183
env 335
pol 455
pol 538
pol 562
Epitope

FIG.29B

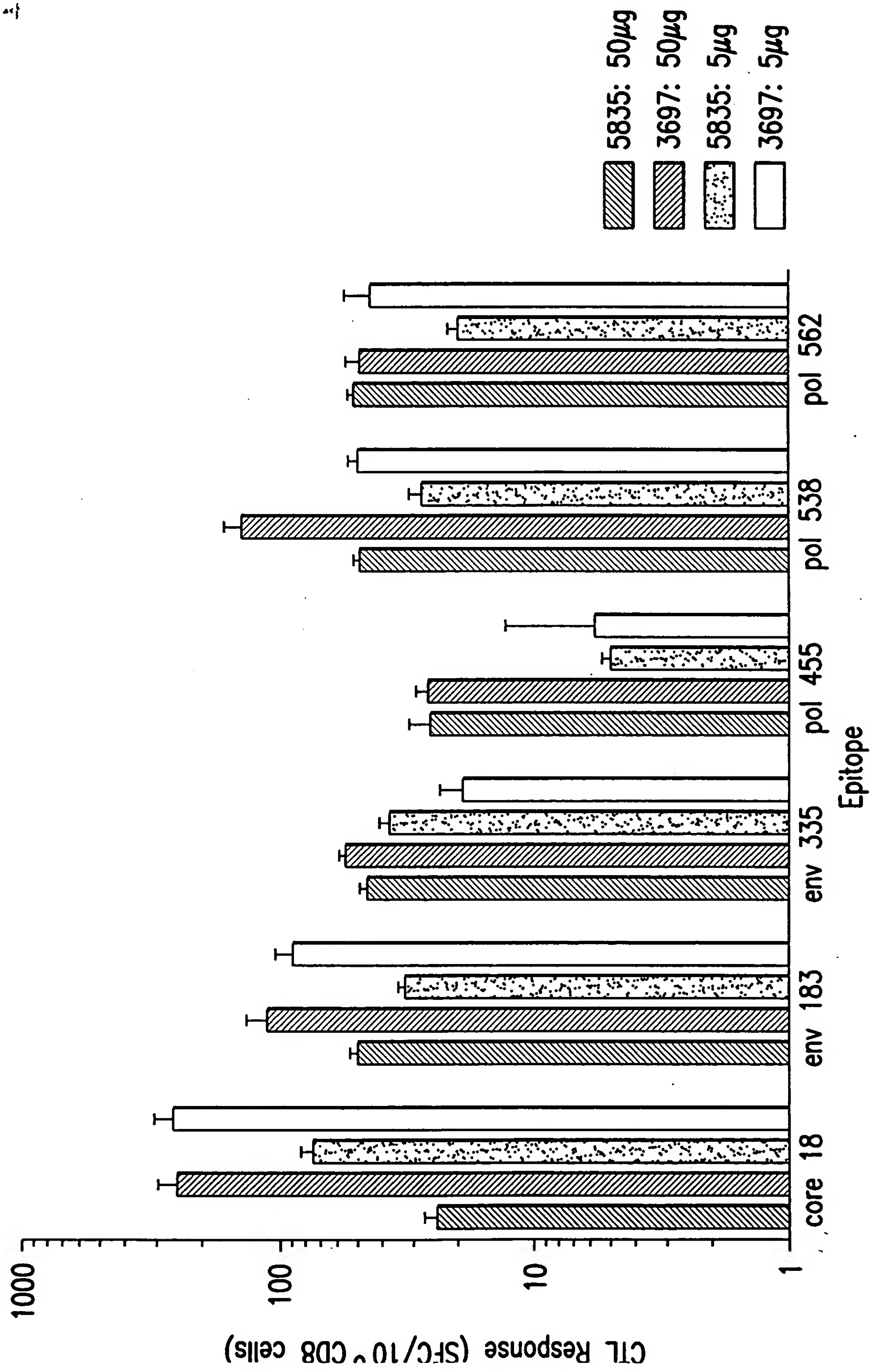

5835: 50μg
3697: 50μg
5835: 5μg
3697: 5μg
CTL Response (SFC/10^6 CD8 cells)
1000
100
10
1
core 18
env 183
env 335
pol 455
pol 538
pol 562
Epitope

FIG.30

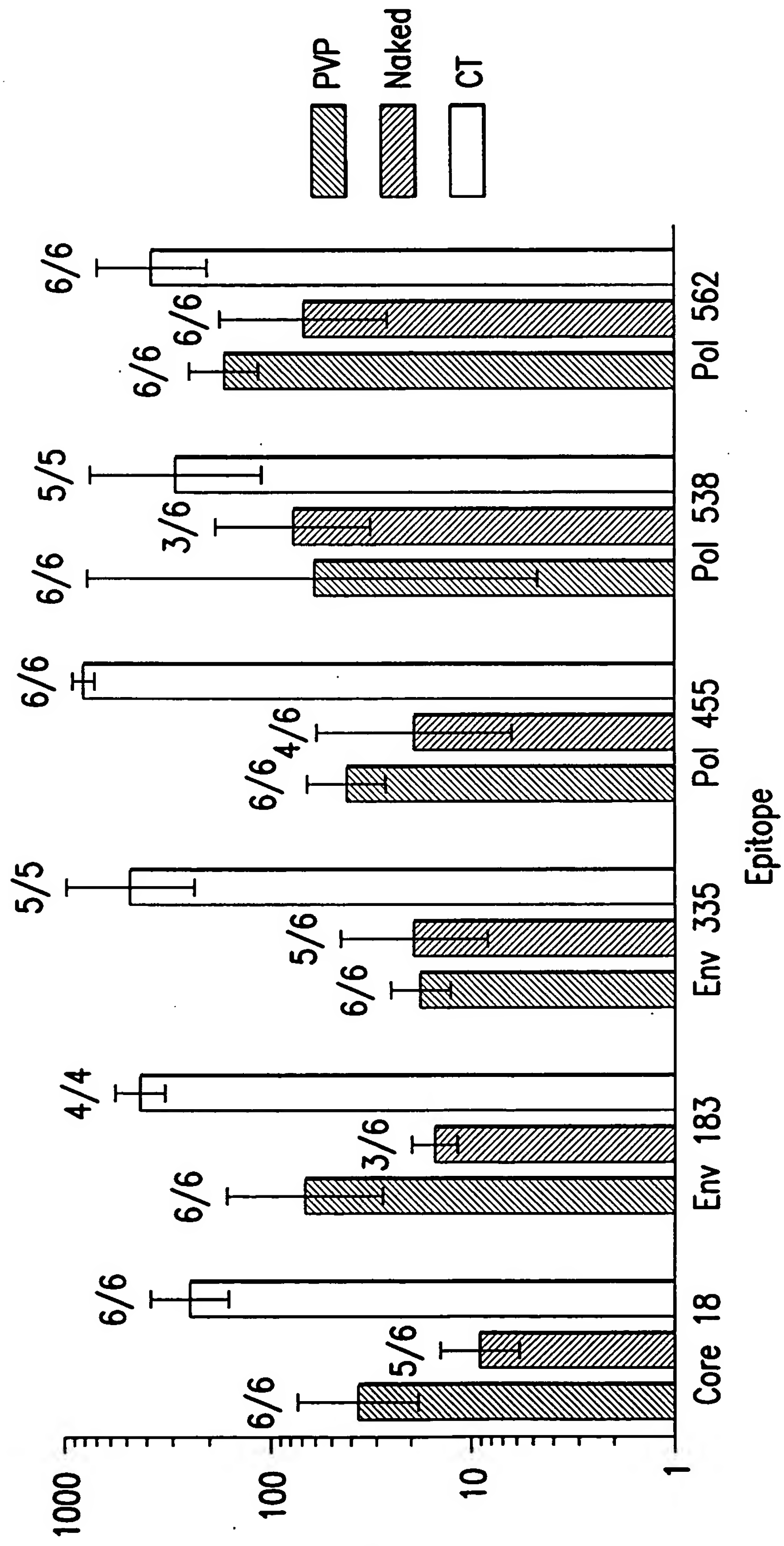

PVP
Naked
CT
1000
100
10
1
6/6
5/6
6/6
6/6
3/6
4/4
6/6
5/6
5/5
6/6
4/6
6/6
6/6
3/6
5/5
6/6
6/6
6/6
Core 18
Env 183
Env 335
Pol 455
Pol 538
Pol 562
Epitope

FIG.31

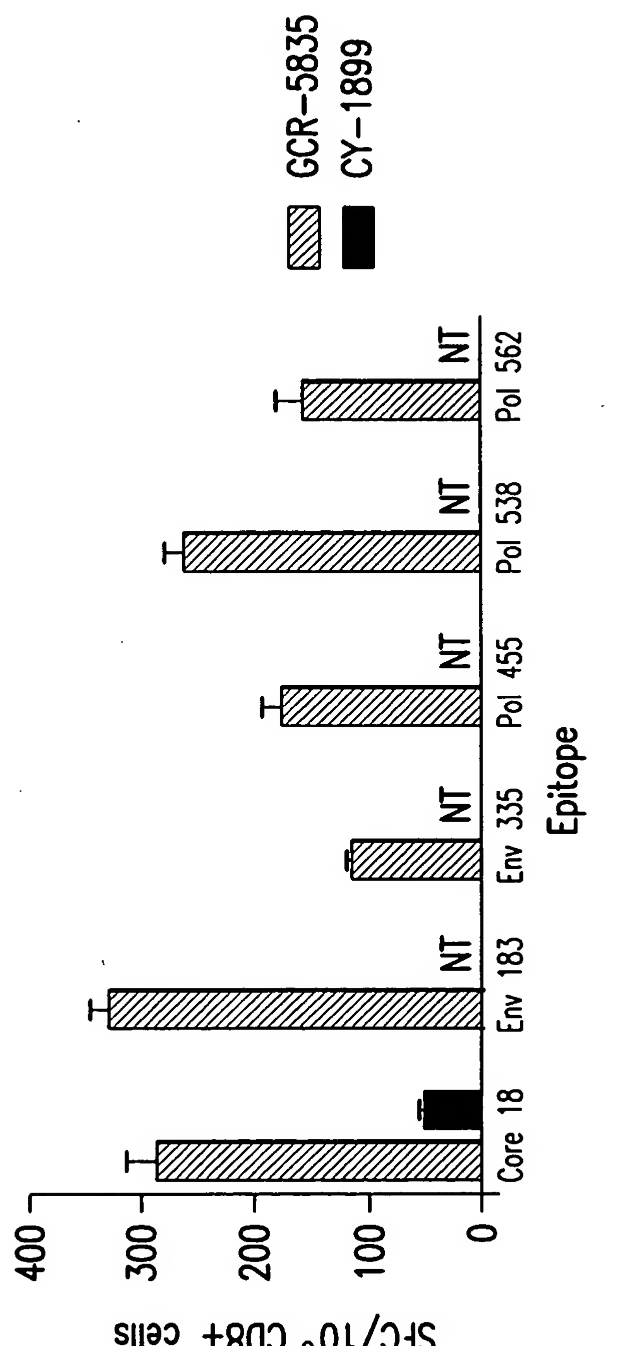


FIG.32A

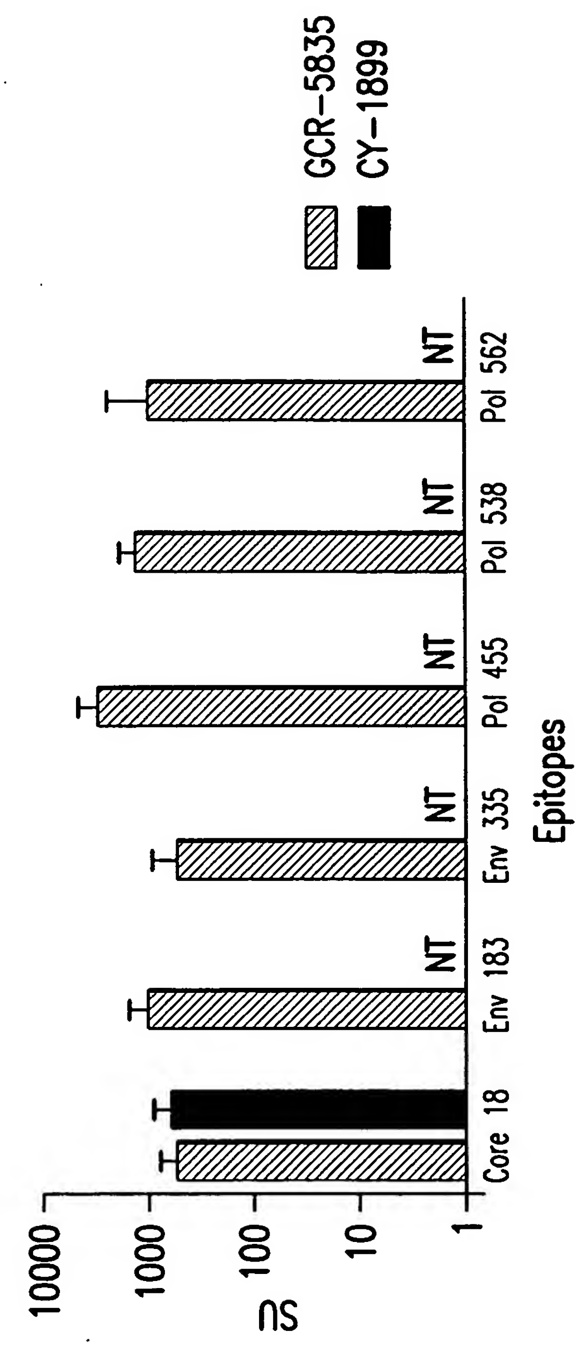


FIG.32B

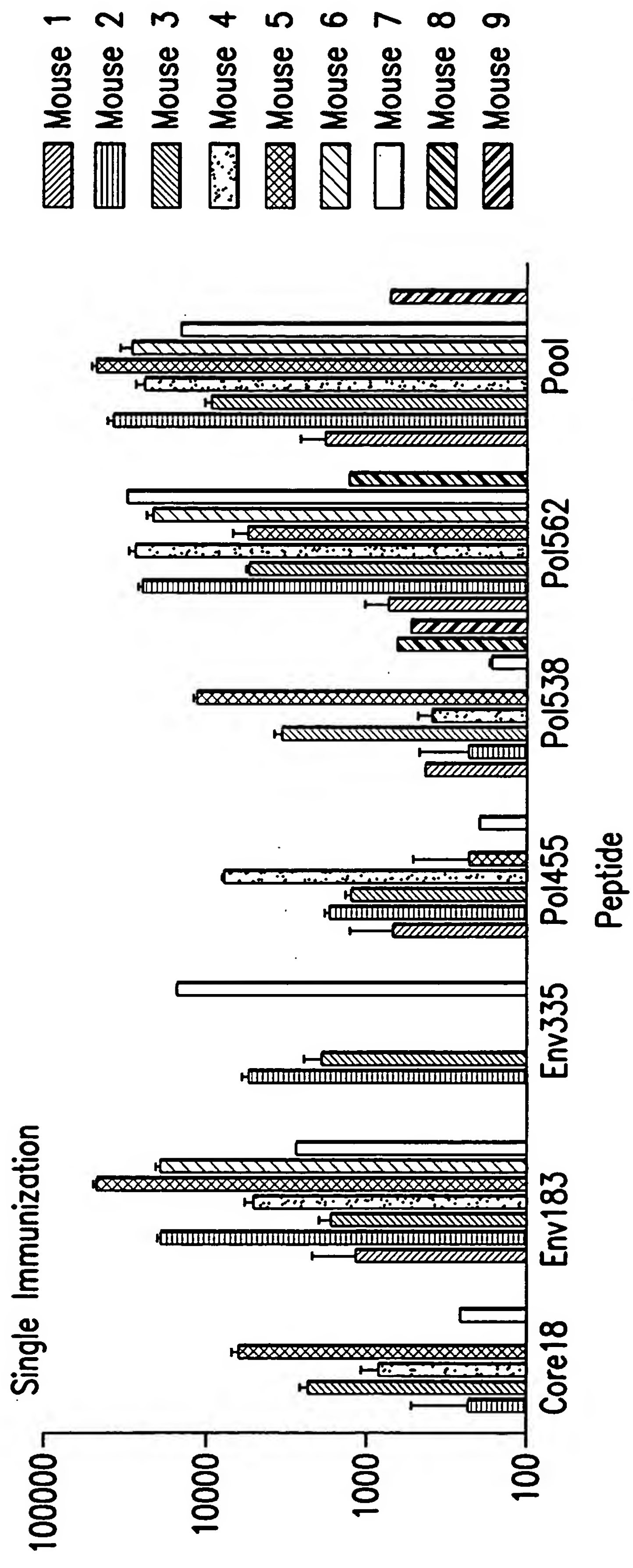

Single Immunization
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8
Mouse 9
100000
10000
1000
100
Core18
Env183
Env335
Pol455
Pol538
Pol562
Pool
Peptide

FIG.33A

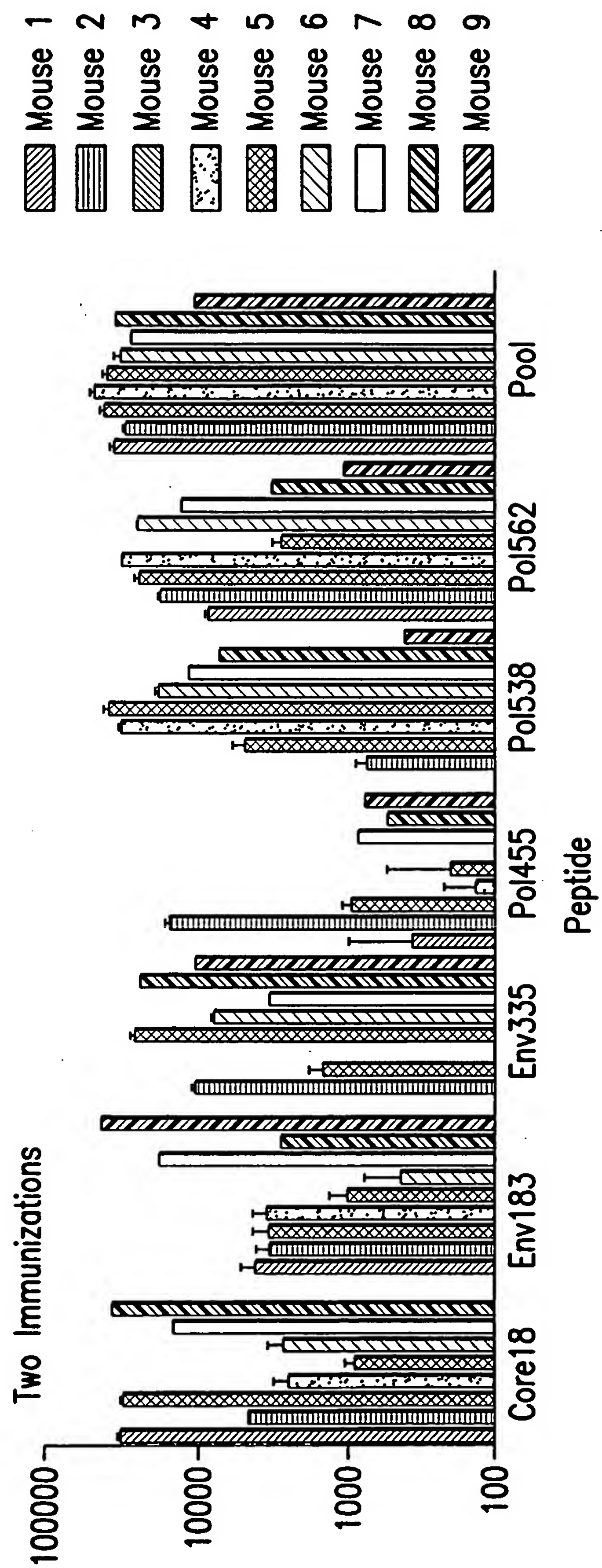

Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8
Mouse 9
Two Immunizations
100000
10000
1000
100
Core18
Env183
Env335
Pol455
Pol538
Pol562
Pool
Peptide

FIG.33B

Composition of HBV polyepitope vaccine

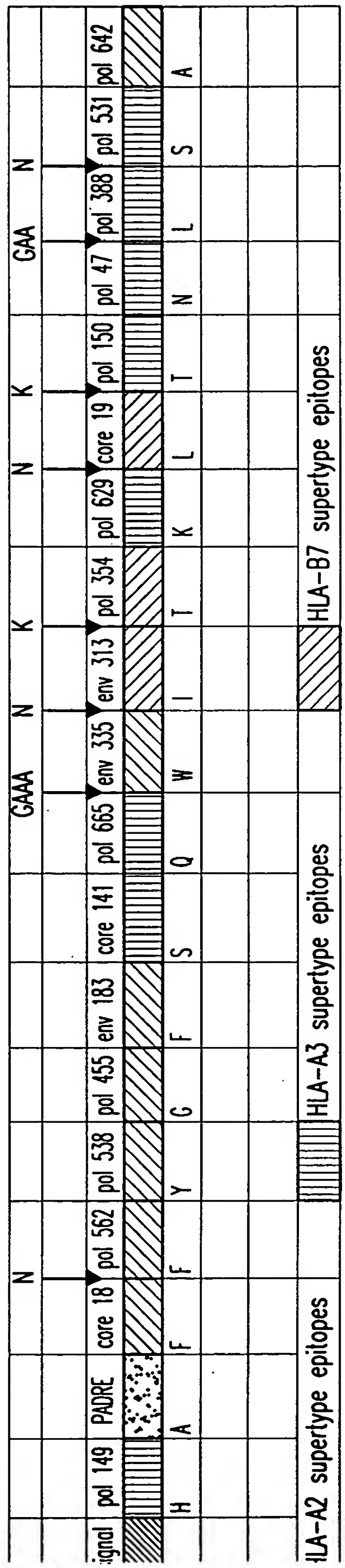


FIG.34

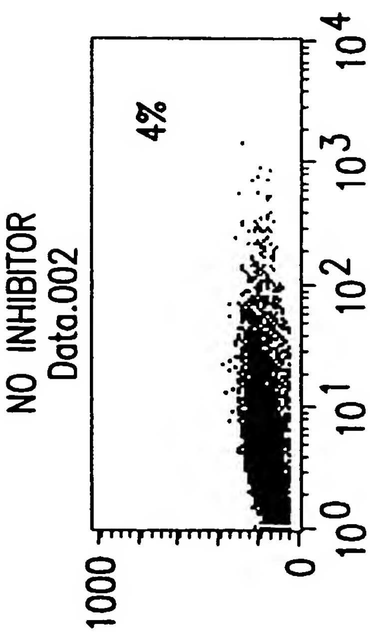


FIG.35A-1

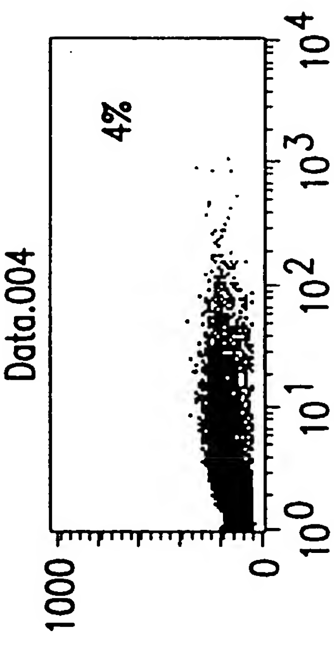


FIG.35A-2

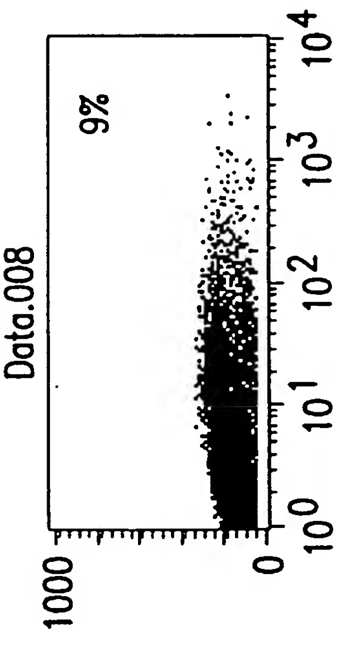


FIG.35A-3

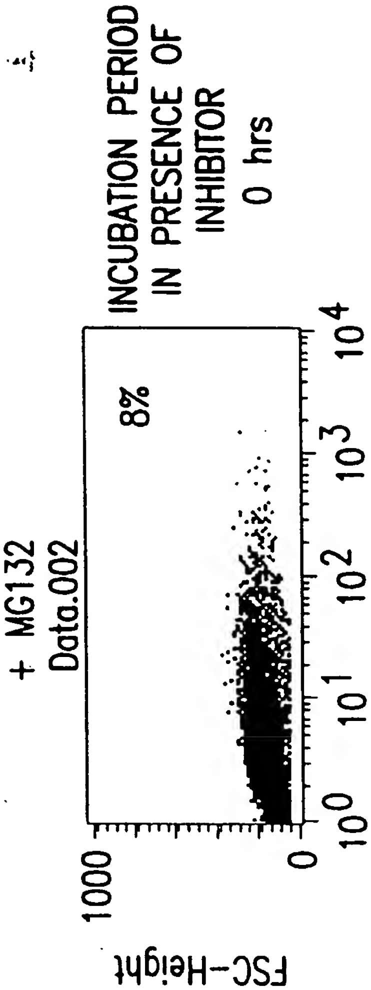


FIG.35A-4

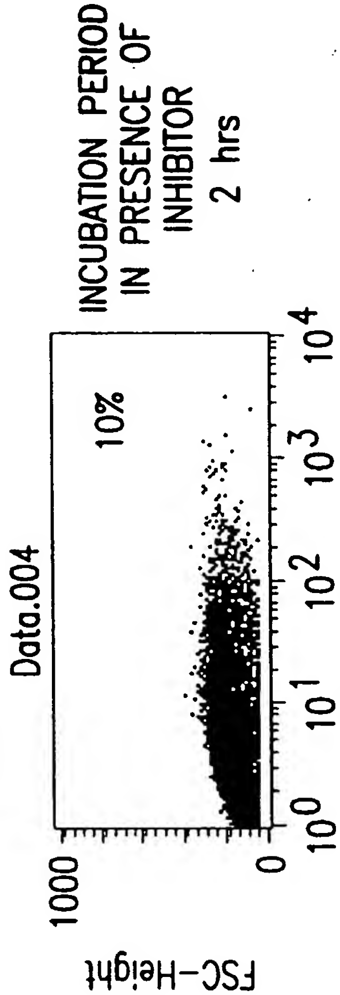


FIG.35A-5

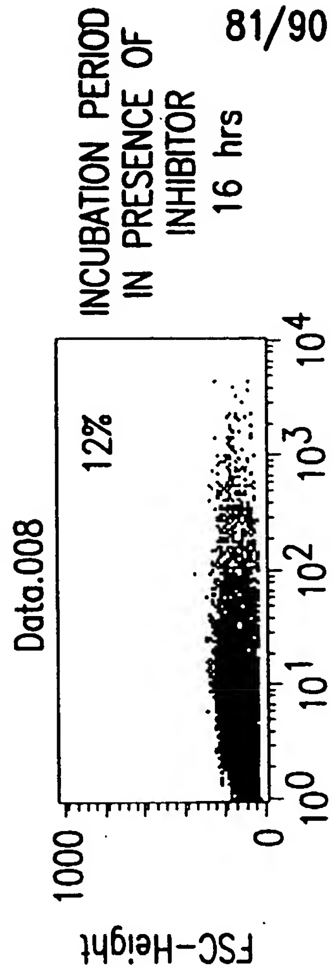


FIG.35A-6

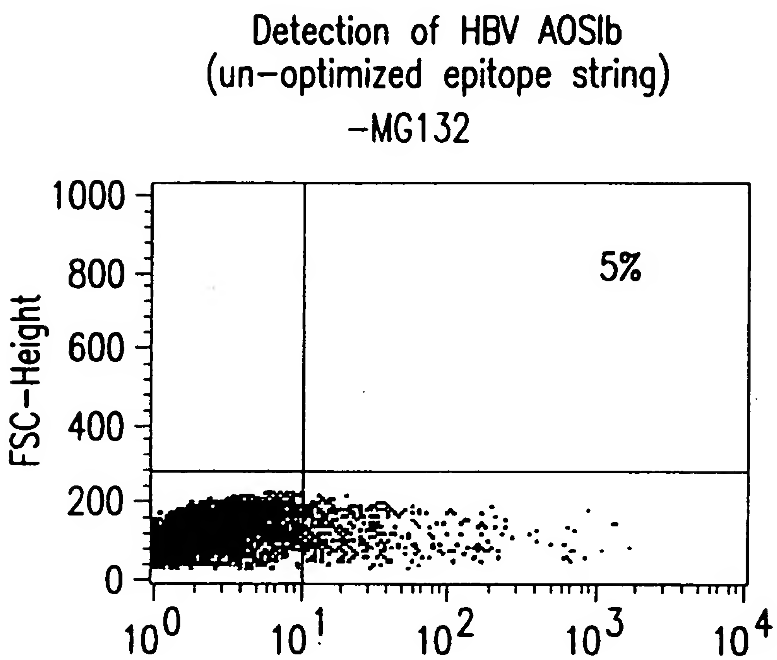


FIG.35B-1

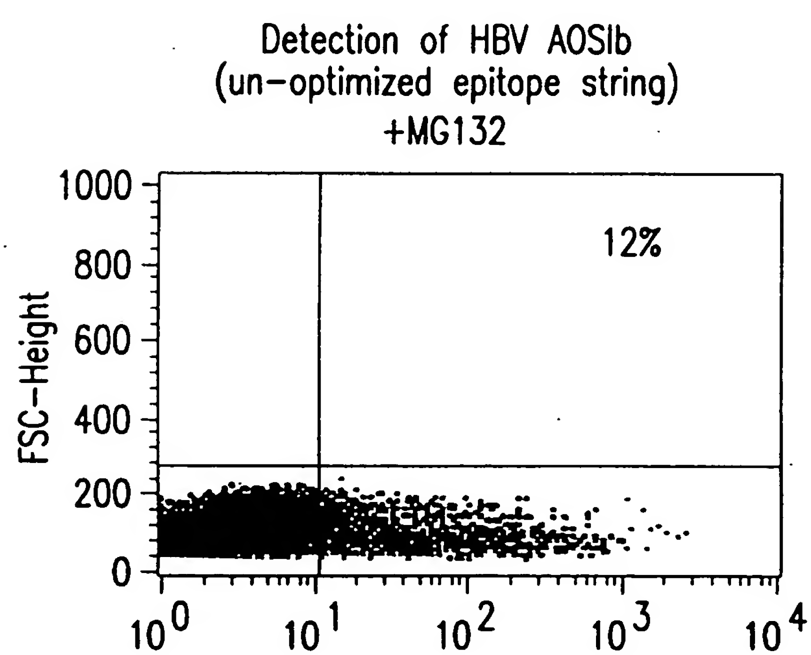


FIG.35B-2

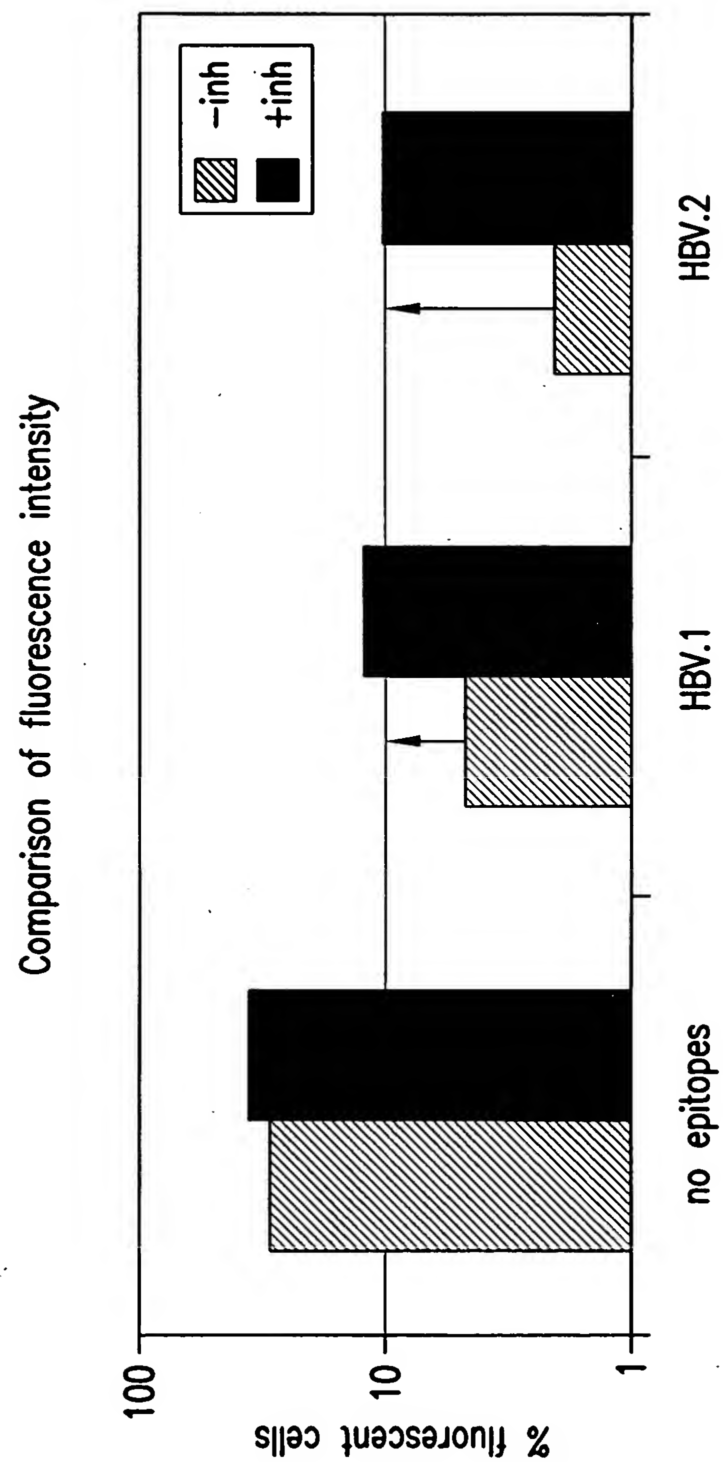

Comparison of fluorescence intensity
% fluorescent cells
100
10
1
-inh
+inh
no epitopes
HBV.1
HBV.2

FIG.35D

plasmid	No inhibitor	with inhibitor	Fold Increase (aver.)
Fluorescent Protein (no epitopes control)	30% 34%	35% 33%	1.1
HBV AOSIb fusion	5% 4.4	12% 8%	2.1
HBV AOSIb2 fusion	2% 1.2%	10% 6.6	5.3

FIG.35E

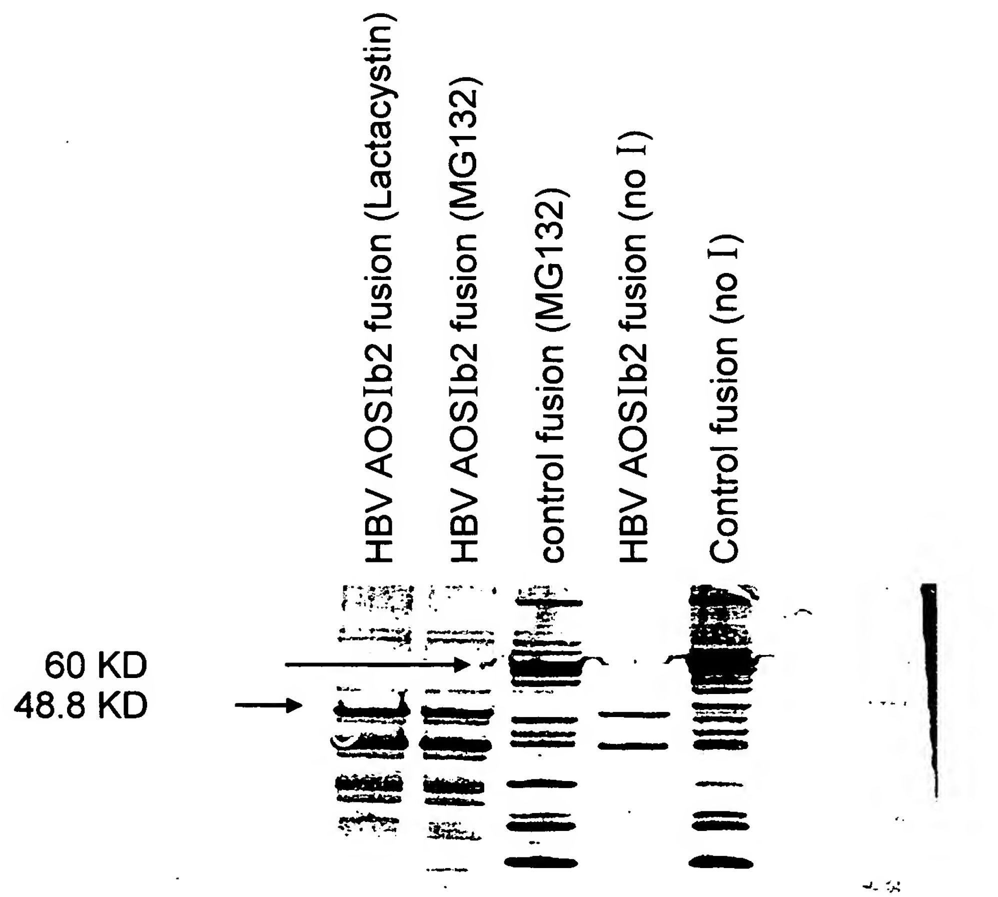

HBV AOSIb2 fusion (Lactacystin)
HBV AOSIb2 fusion (MG132)
control fusion (MG132)
HBV AOSIb2 fusion (no I)
Control fusion (no I)
60 KD
48.8 KD

FIG.36

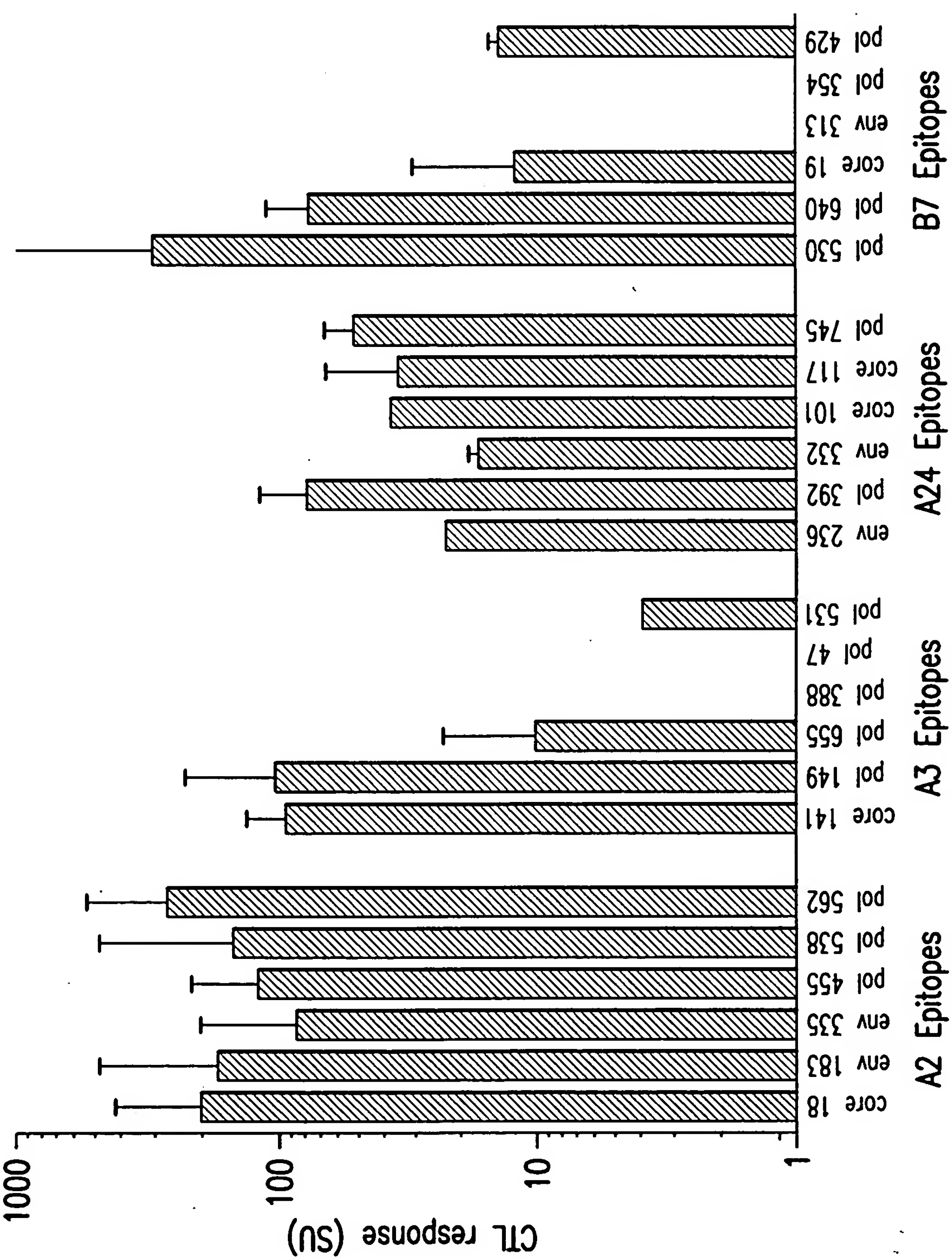

CTL response (SU)
1000
100
10
1
core 18
env 183
env 335
pol 455
pol 538
pol 562
A2 Epitopes
core 141
pol 149
pol 655
pol 388
pol 47
pol 531
A3 Epitopes
env 236
pol 392
env 332
core 101
core 117
pol 745
A24 Epitopes
pol 530
pol 640
core 19
env 313
pol 354
pol 429
B7 Epitopes

FIG.37A

GCR-3697 Immunogenicity Data

HLA Supertype	Epitope	CTL response (SU): 2 x PVP Immunization Freq.	GeoMean	X/÷	CT Pre-treatment Freq.	GeoMean	X/÷
HLA-A2	core 18	12/12	199.3	2.1	4/4	288.9	1.3
	env 183	12/12	171.2	2.8	4/4	401.2	1.4
	env 335	12/12	86.4	2.3	4/4	153.6	1.7
	pol 455	12/12	120.4	1.8	4/4	411.3	1.8
	pol 538	12/12	149.9	3.2	4/4	148.1	2.2
	pol 562	12/12	266.2	2	4/4	353.3	1.5
HLA-A3	core 141	6/6	94.4	1.4	12/12	167.6	1.4
	pol 149	6/6	103	2.2	12/12	386.7	1.5
	pol 655	5/6	10.1	2.3	12/12	108	3.6
	pol 388	0/6			0/12		
	pol 47	0/6			3/12	3.2	1.1
	pol 531	1/6	3.9		2/12	5.5	1
HLA-A24	env 236	1/6	22.6		2/11	23.4	1.2
	pol 392	5/6	78.1	1.5	10/11	54.8	2.2
	env 332	2/6	16.7	1.1	3/11	25.6	1.6
	core 101	1/6	37		0/11		
	core 117	3/6	34.4	1.9	2/11	27.4	3
	pol 745	2/6	51.2	1.3	1/11	32.6	
HLA-B7	pol 530	6/6	292.4	3.1	3/6	177	1.3
	pol 640	4/6	76.5	1.7	5/7	104.6	1.8
	core 19	3/6	12	2.5	2/7	8.8	1.6
	env 313	0/6	0	0	6/6	323.1	2.9
	pol 354	0/6	0	0	4/6	351.5	3.2
	pol 429	2/6	13.7	1.1	1/6	1.4	

FIG.37B